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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-  
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION  
PROTEIN KINASES

FIELD OF THE INVENTION

5           The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10           The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

          Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key  
15           biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

          Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:  
20           cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the  
25           etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

          The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism  
30           includes changes in the catalytic properties ( $V_{\max}$  and  $K_m$ ) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

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ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex  
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important  
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several  
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple  
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca<sup>2+</sup>/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain  
10 kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the  
25 yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close  
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD\_sp, YGR262\_sc) kinases, and others that are "unique" and don't cluster into any obvious family.



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### SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting

SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

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5 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides  
conjugated to each other, including DNA and RNA, that is isolated from a natural source  
10 or that is synthesized. The isolated nucleic acid of the present invention is unique in the  
sense that it is not found in a pure or separated state in nature. Use of the term "isolated"  
indicates that a naturally occurring sequence has been removed from its normal cellular  
(i.e., chromosomal) environment. Thus, the sequence may be in a cell-free solution or  
placed in a different cellular environment. The term does not imply that the sequence is  
15 the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at  
least) of non-nucleotide material naturally associated with it, and thus is distinguished  
from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the  
specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of  
20 the total DNA or RNA present in the cells or solution of interest than in normal or  
diseased cells or in the cells from which the sequence was taken. This could be caused by  
a person by preferential reduction in the amount of other DNA or RNA present, or by a  
preferential increase in the amount of the specific DNA or RNA sequence, or by a  
combination of the two. However, it should be noted that enriched does not imply that  
25 there are no other DNA or RNA sequences present, just that the relative amount of the  
sequence of interest has been significantly increased. The term "significant" is used to  
indicate that the level of increase is useful to the person making such an increase, and  
generally means an increase relative to other nucleic acids of about at least 2 fold, more  
preferably at least 5 to 10 fold or even more. The term also does not imply that there is no  
30 DNA or RNA from other sources. The other source DNA may, for example, comprise  
DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term  
distinguishes from naturally occurring events, such as viral infection, or tumor type

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growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

5 It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The  
10 claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from  
15 the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately  $10^6$ -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

20 By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
25 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
30 SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

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The amino acid sequence will be substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID

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NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding  
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially  
similar to a sequence selected from the group consisting of those set forth in SEQ ID  
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NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%  
15 and most preferably 99-100%) to a sequence selected from the group consisting of those  
set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ  
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30 ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ  
ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ  
ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ

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ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 or portions of or the entire corresponding full-length amino acid sequences.

By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
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ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
5 ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
10 ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ  
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ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ  
ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ  
ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ  
20 ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length  
amino acid sequence, or fragments thereof. A sequence that is substantially similar to a  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
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25 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
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NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID



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NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID

NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
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NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
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5 NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c)  
10 hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes  
a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an  
amino acid sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
15 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
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NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
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NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID  
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID  
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID  
25 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID  
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID  
NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
30 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
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NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

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NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
5 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID  
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID  
10 NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
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NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID  
15 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
20 NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
25 ID NO:242, except that it lacks one or more, but not all, of a domain selected from the  
group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a  
coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-  
terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a  
polypeptide having an amino acid sequence selected from the group consisting of those set  
30 forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID  
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID  
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

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NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID  
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID  
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID  
5 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID  
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID  
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID  
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID  
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
10 NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID  
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
15 NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95%  
and most preferably 99-100%) to the sequence selected from the group consisting of those  
20 set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ  
ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ  
ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ  
ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ  
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ  
25 ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ  
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ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ  
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ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ  
ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

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ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of

those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,



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SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

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of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID  
NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID  
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NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID  
5 NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID  
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID  
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15 NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID  
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID  
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20 NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID  
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NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID  
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID  
25 NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino  
acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence  
selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
30 SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
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SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
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5 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
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SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
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SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at  
20 least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-  
100%) to the sequence selected from the group consisting of those set forth in SEQ ID  
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
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NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID  
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NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID  
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

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5 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID  
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID  
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID  
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NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID  
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID  
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID  
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under  
15 highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally  
occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
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20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
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25 NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
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NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
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NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID  
5 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID  
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID  
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID  
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID  
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the  
10 corresponding full-length amino acid sequence, or fragments thereof. A sequence that is  
substantially similar to a sequence selected from the group consisting of those set forth in  
SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126,  
SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131,  
SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,  
15 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
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25 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
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30 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
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SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

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complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) *J. Biol. Chem.* 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further,  
10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate  
20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine  
25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of  
30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal



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domain may play a regulatory role is PAK3 which contains a heterotrimeric G<sub>i</sub> subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic  $\alpha$ -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

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sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein-protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).

Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

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The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM  $\text{NaH}_2\text{PO}_4$ , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

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vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID  
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ  
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative  
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
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20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID  
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID  
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID  
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID  
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID  
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

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NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,



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SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.  
25 In particular, a unique nucleic acid region is preferably of mammalian origin and  
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of  
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is  
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,  
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid  
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino  
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,  
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,  
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,  
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,  
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,  
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,  
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,  
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,  
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,  
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,

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SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,  
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,  
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,  
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,  
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe  
contains a nucleotide base sequence that will hybridize to a sequence selected from the  
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ  
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,  
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ  
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID  
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,  
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ  
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID  
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,  
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ  
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID  
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,  
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ  
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID  
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,  
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

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NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the  
genomic regulatory elements, or may be under the control of exogenous regulatory  
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is  
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase  
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid  
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID  
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID  
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID  
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID  
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID  
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID  
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID  
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID  
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID  
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID  
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID  
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID  
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID  
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID  
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

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NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-  
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase  
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ  
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ  
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ  
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ  
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ  
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ  
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ  
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ  
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ



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ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (e.g., in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, 10 20 25 30 the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

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amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

5 ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ  
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ  
ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ  
ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ  
ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ  
ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ  
ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ  
ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ  
ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ  
10 ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ  
ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ  
ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ  
ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ  
ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ  
15 ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ  
ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ  
ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ  
ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ  
ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ  
20 ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ  
ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ  
ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
25 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ  
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
30 ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

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ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242 where the domain is selected from the group consisting of an N-terminal domain,  
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich  
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence  
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,  
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,  
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,  
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,  
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,  
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,  
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,  
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,  
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,  
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

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SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
5 SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it  
lacks one or more, but not all, of the domains selected from the group consisting of a C-  
terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich  
10 region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain  
demarcations of the polypeptides of the invention are indicated in Table 2 by reference to  
the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in  
the art. The natural source may be mammalian, preferably human, blood, semen, or tissue,  
15 and the polypeptide may be synthesized using an automated polypeptide synthesizer. The  
isolated, enriched, or purified kinase polypeptide is preferably selected from the group  
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
20 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ  
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
25 ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
30 ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,



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SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By "specific binding affinity" is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term "specific binding affinity" describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term "polyclonal" refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

"Monoclonal antibodies" are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term "antibody fragment" refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

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kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

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SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
NO:242. The binding agent is preferably a purified antibody that recognizes an epitope  
present on a kinase polypeptide of the invention. Other binding agents include molecules  
that bind to kinase polypeptides and analogous molecules that bind to a kinase  
15 polypeptide. Such binding agents may be identified by using assays that measure kinase  
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a  
kinase polypeptide of the invention or an equivalent sequence. The method involves  
identifying the novel polypeptide in human cells using techniques that are routine and  
20 standard in the art, such as those described herein for identifying the kinases of the  
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR  
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that  
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide  
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,  
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,  
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,  
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,  
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,  
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,  
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,  
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,  
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,  
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,  
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,  
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,  
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,  
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,  
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,  
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,  
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,  
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,  
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,  
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,  
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,  
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,  
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,  
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)  
measuring the activity of said polypeptide; and (c) determining whether said substance  
modulates the activity of said polypeptide.

20 The term "modulates" refers to the ability of a compound to alter the function of a  
kinase of the invention. A modulator preferably activates or inhibits the activity of a  
kinase of the invention.

The term "activates" refers to increasing the cellular activity of the kinase. The  
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is  
25 preferably the interaction with a natural binding partner.

The term "modulates" also refers to altering the function of kinases of the  
invention by increasing or decreasing the probability that a complex forms between the  
kinase and a natural binding partner. A modulator preferably increases the probability that  
such a complex forms between the kinase and the natural binding partner, more preferably  
30 increases or decreases the probability that a complex forms between the kinase and the  
natural binding partner depending on the concentration of the compound exposed to the

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kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

5 The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

10 The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

15 The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

20 In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, 25 SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, 30 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change  
in cell phenotype or the interaction between said polypeptide and a natural binding  
partner.

The term "expressing" as used herein refers to the production of kinases of the  
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic  
20 acid vector is transfected into cells using well known techniques in the art as described  
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal  
condition by administering to a patient in need of such treatment a substance that  
modulates the activity of a polypeptide selected from the group consisting of SEQ ID  
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID  
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID  
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID  
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID  
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID  
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID  
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID  
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID



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NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

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preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term "preventing" refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term "treating" refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

The term "therapeutic effect" refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of  
10 abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating  
15 efficacy against abnormal conditions can be identified as described herein.

The term "abnormal condition" refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in  
20 normal cell cycle progression through mitosis and meiosis.

Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

Abnormal differentiation conditions include, but are not limited to  
25 neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the  
30 protein kinases could lead to cell immortality or premature cell death.

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The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

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5 ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ  
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ  
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ  
ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ  
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ  
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ  
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ  
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ  
ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ  
10 ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ  
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ  
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ  
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ  
ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ  
15 ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ  
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ  
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe  
comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the  
complements of the sequences and fragments; and (b) detecting the presence or amount of  
20 the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from  
the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, organ  
transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative  
stress-related neurodegenerative disorders, metabolic disorder including diabetes,  
25 reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group  
consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID  
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ  
ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID  
30 NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20,  
SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ  
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

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NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID  
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID  
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID  
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID  
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID  
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID  
NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID  
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID  
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID  
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID  
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID  
NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID  
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID  
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding  
full-length amino acid sequence, or a functional derivative thereof. Hybridization  
conditions should be such that hybridization occurs only with the kinase genes in the  
presence of other nucleic acid molecules. Under stringent hybridization conditions only  
highly complementary nucleic acid sequences hybridize. Preferably, such conditions  
prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20  
contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the  
genes in the presence of other nucleic acid molecules. Under stringent hybridization  
conditions only highly complementary nucleic acid sequences hybridize. Preferably, such  
conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20  
contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic  
include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in  
comparison to normal cells. By "amplification" is meant increased numbers of kinase

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DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

"Amplification" as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon



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& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative  
10 publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5,316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris  
15 *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,  
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated  
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432  
30 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., "J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

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formulated in animal models to achieve a circulating concentration range that initially takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in  
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

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NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting  
5 differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include,  
10 but are not limited to, those discussed previously.

The term "comparing" as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine  
15 these discrepancies in sequences are well-known to one of ordinary skill in the art. The "control" nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the  
20 narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred  
25 embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

### BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

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NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

### I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID



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NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide or polynucleotide may be used in this regard, provided that its addition, deletion or substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,  
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,  
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,  
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,  
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,  
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,  
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,  
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,  
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,  
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,  
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,  
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,  
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,  
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,  
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,  
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded  
by the nucleotide sequence. For example, the present invention is intended to include any  
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-  
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,  
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or  
its derivative. Moreover, the nucleic acid molecule of the present invention may, as  
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-  
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity  
25 to promote secretion and/or processing of heterologous proteins encoded by foreign  
nucleic acid sequences fused thereto, for example. All variations of the nucleotide  
sequence of the kinase genes of the invention and fragments thereof permitted by the  
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with  
30 codons other than degenerate codons to produce a structurally modified polypeptide, but  
one which has substantially the same utility or activity as the polypeptide produced by the  
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

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functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5           Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.  
10          Therefore, these nucleic acid molecules are also part of the invention.

          The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore  
15          presumably define new protein kinase groups.

          Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

## 20          II.     Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

          A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,  
25          Sambrook, Fritsch, & Maniatis, eds., 1989).

          In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain  
30          reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

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radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

### III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

5 A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the  
10 regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of  
15 transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and  
20 polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence  
25 encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the  
30 promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

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Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells. Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include  $\gamma$ gt10,  $\gamma$ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage  $\lambda$ , the *bla* promoter of the  $\beta$ -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage  $\lambda$  ( $P_L$  and  $P_R$ ), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the  $\alpha$ -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the  $\zeta$ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).



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Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK-promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

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the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184,  $\pi$ VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as  $\phi$ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

#### IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any  
5 organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

10 Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

15 One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that  
20 can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,  
25 SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167,  
30 SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

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SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,  
 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,  
 SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,  
 SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,  
 5 SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,  
 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,  
 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,  
 SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,  
 SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,  
 10 SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,  
 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,  
 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID  
 NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of  
 these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-  
 15 terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are  
 provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI,  
 CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant  
 number of protein kinases that do not belong to any of the known groups, and therefore  
 20 presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1,  
 Table 2, Table 3 and Table 4, provided below.

#### V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein 25 Kinases

The present invention relates to an antibody having binding affinity to a kinase of  
 the invention. The polypeptide may have an amino acid sequence selected from the group  
 consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ  
 ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ  
 30 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ  
 ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ  
 ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

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5 ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ  
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ  
ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ  
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ  
ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ  
ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ  
ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ  
ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ  
ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ  
10 ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ  
ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ  
ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ  
ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ  
ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ  
15 ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ  
ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ  
ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ  
ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ  
ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ  
20 ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or  
at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more  
contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the  
polypeptide not provided in the sequences above, but that is present in the full-length  
sequence of the polypeptide and that is easily obtained using methods standard in the art.  
25 Further, the antibody may bind specifically to particular domains of one or more of the  
kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or  
C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to  
a kinase or kinase domain of the invention. Such an antibody may be isolated by  
30 comparing its binding affinity to a kinase of the invention with its binding affinity to other  
polypeptides. Those that bind selectively to a kinase of the invention would be chosen for  
use in methods requiring a distinction between a kinase of the invention and other

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polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

5 The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

10 The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

15 The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

20 In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

25 The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization.

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For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.



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Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

#### VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

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The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions  
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit  
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S.  
20 Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

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Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

## VII. Biological Significance, Applications and Clinical Relevance of Novel Protein

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### Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or therapeutic utility for each of the proteins.

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The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune, neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

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The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatinum, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

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Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5       Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

      Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

      Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15       Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

      Neuronal restricted: CAMKKB (SEQ ID NO:66)

      Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20       Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP\_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

      Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

#### VIII. Transgenic Animals.

30       A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (*Experientia* 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO<sub>2</sub> asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, *Cell* 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.



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Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

#### IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

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1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is  
10 precipitated with  $\text{CaPO}_4$  and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and  
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to  
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic acid molecule into a cell. Gene transfer is commonly performed to enable the expression  
25 of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or  
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

#### X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

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takes into account the  $IC_{50}$  as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

5 Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by  
10 altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used);  
15 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

20 At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross  
25 necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

### EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

#### EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

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Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

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Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

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with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATIT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAAC GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATT TGAAAAAT	CTTCATCATCTCTAATACAT TGGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

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#### Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

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PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flt	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

5

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

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The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

#### Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the *evc* (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1\_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D. (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- $\kappa$ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceeded by the sequence

25 "RGLLAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

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region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102  
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM\_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1 ) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM\_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324\_h orthologue of W30246\_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP\_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119\_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

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refer to the aa sequence of the closest homolog (RU2S, NP\_057440) used for the Smith-Waterman query): N-term from Incyte 6010175\_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175\_2, Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three  
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to  
15 encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838\_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from  
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735\_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135\_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte  
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on  
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

5 Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015\_m (SEQ ID NO: 42, SEQ ID NO:162)

10 tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

15 The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

20 Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

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				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

\* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3\_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

25 Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344\_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)



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Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478\_m (SEQ ID NO:80, SEQ ID NO:199)

5 Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

10 The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

15 Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

\* C-terminus specific to MLK4B

17 LPLAARMSEESYFESKTEESNSAEMSCQITATSNAGEGHGMNPSLQAMMLMGFGDI  
18 FSMNKAGAVMHSGMQINMQAKQNSS  
20 KTTSKRRGKKVNMA LGFSDFDLSEGDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

25 Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15 Human SGK022 orthologue of AA060026\_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20 Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence 1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25 Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

30 Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP\_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP\_h 6921333\_9; removed intron (146-893) predicted from blastx analysis.

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Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.T and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG\_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was  
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601\_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF  
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG\_040010.

Human orthologue of AA671275\_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related  
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

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Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase 6 (MAP3K6) (NM\_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

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78	92
79	93
80	94
157	193

### Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR  
5 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press  
10 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu,  
15 LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR  
20 fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press  
25 (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca <sup>2+</sup> /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

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SGK      Serum and glucocorticoid-regulated kinase  
STK      serine threonine kinase  
ULK      UNC-51-like kinase

The following abbreviations were used for species

H      Human  
M      Murine  
R      Rat  
FV      Fowlpox virus  
MT      *M. thermoautotrophicum*  
CE      *Caenorhabditis elegans*  
DM      *Drosophila melanogaster*  
OS      *Oryza sativa*  
SP      *Schizosaccharomyces pombe*  
TP      *Tetrahymena pyriformis*  
PI      *Petunia inflata*  
NC      *Neurospora crassa*  
MSV      *Medicago sativa*  
MSV      Moloney murine sarcoma virus  
SA      *Squalus acanthias*  
CS      *Cucumis sativus*  
GM      *Glycine max*  
LL      *Lilium longiflorum*  
TV      *Trichomonas vaginalis*  
MP      *Mycoplasma pneumoniae*  
DD      *Dictyostelium discoideum*  
SC      *Saccharomyces cerevisiae*  
MT      *Methanobacterium thermoautotrophicum*





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### Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program ([www.ch.embnet.org/software/COILS\\_form.html](http://www.ch.embnet.org/software/COILS_form.html)). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind ([www.at.embnet.org/embnet/tools/bio/PESTfind/](http://www.at.embnet.org/embnet/tools/bio/PESTfind/)). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) *Science* 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

### **Identification of potential coiled-coil domains and PEST domains in N34132**

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

5 Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

## 10 EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

### Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map ([http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts\\_info?database=release](http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release)). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

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following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at

5 [http://www.ncbi.nlm.nih.gov/BLAST/blast\\_databases.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html)) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above,

10 Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the

15 entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline

20 (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

### Results

25 The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with

30 chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)  
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

### EXAMPLE 3: Generation of Specific Immunoreagents

#### Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TECLKRSQDLPREPLP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

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AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRS	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVKED	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSISTissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon membranes and probed with 32P-labeled cDNA fragments derived from the gene(s) of interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at each end. An oligo dT primer containing a specific sequence (CDS:  
AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals to the added Cs and the MMLV recognizes the rest of the primer sequence as template and continues transcription. As a result, the synthesized cDNAs contain specific sequence tags at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric.” A double-stranded “cDNA library” is then generated by PCR amplification using the 3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2: AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech) and hybridized with 32P labeled probes generated by random hexamer priming of cDNA fragments corresponding to the genes of interest. After washing, the blots were exposed to phosphorimaging cassettes and the intensity of the signal was quantified. The amount of the DNA on the arrays was also quantified by treating non-denatured or denatured arrays with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2 minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

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with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

## 5      Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRJ), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AIG86865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

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EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

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Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

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EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

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Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.



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### CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

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What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

(c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

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(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

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5 NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID  
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID  
NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID  
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID  
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID  
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID  
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID  
NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID  
NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID  
10 NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID  
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID  
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID  
NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID  
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID  
15 NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID  
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID  
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID  
NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID  
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID  
20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID  
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID  
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID  
NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not  
all, of the domains selected from the group consisting of an N-terminal domain, a catalytic  
25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure  
region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or  
promoter effective to initiate transcription in a host cell.

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4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of  
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
10 SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,  
15 SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.



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7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, ~~SEQ ID NO:128~~, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

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9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

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11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
5 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
10 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
15 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
20 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

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ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

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NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID  
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID  
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting  
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a  
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

15 13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated,  
purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090,  
20 N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515,  
AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215,  
AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936,  
W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838,  
25 W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-  
1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859,  
30 AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a  
AA631990 or W08549 polypeptide.



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20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

15 25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

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26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

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5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ  
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ  
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ  
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ  
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ  
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ  
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ  
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ  
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ  
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ  
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ  
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ  
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ  
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ  
25 ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ  
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and  
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ  
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ  
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ  
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ  
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ  
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ  
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ  
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ  
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ  
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

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ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

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NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID  
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID  
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID  
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID  
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID  
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID  
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID  
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID  
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID  
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID  
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID  
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting  
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a  
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

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28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

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SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,  
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,  
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,  
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,  
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,  
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,  
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,  
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,  
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,  
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,  
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,  
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,  
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,  
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,  
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,  
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,  
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,  
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,  
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,  
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,  
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,  
and SEQ ID NO:242 with a test substance;

- (b) measuring the activity of said polypeptide; and
  - (c) determining whether said substance modulates the activity of said
- 25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a cell comprising:

- (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
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5 NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID  
NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID  
NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID  
NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID  
10 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID  
NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID  
NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID  
NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID  
NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID  
15 NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID  
NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID  
NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID  
NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID  
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID  
20 NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID  
NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID  
NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID  
NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID  
NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID  
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID  
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between  
said polypeptide and a natural binding partner.



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31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

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(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

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ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

- 5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

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Table 1

Gene Name	SP	Prov	Seq. ID	NA	Prov	Seq. ID	AA	SEQ ID #	na	SEQ ID #	aa	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeat	CHR location
X8117 h, BARK2 h	H							1	122			AGC	GRK	2087	666	1	2084	2084		22q11
AA144374 m, BARK2 m	M							2	123			AGC	GRK	1968	378	2	1955	1954		NA
AA268590 h	H							3	124			AGC	MoSC11.1, ce	1788	418	8	1764	1757	285-304	NA
AA980957 h	H							4	125			AGC	MoSC11.1, ce	3274	414	65	1308	1242		2p11.1
5R7B-46.1 h, TBK1 h	H							5	126			AGC	MoSC11.1, ce	3013	729	93	2279	2187		NA
AA305176 h	H							6	127			AGC	NDR	1421	329	53	1039	987		10p11.2
AA116841 m	M							7	128			AGC	NDR	542	88	3	266	264		NA
AA256100 h	H							8	129			AGC	NDR	4683	164	86	1477	1392		12q11
AA210825 h	H							9	130			AGC	PKC	3263	678	117	3050	2834		18q13-q13.3
AA127269 h	H							10	131			AGC	PKC	315	105	1	315	315		NA
AA316804 h, EPK2	H							11	132			AGC	PKC	2673	880	1	2870	2870		20p1
AA2050 h, PKNbeta	H							12	133			AGC	PKC	2670	889	1	2887	2887	221-2280	NA
AA2050 h, PKNbeta	H							13	134			AGC	PKC	978	205	2	618	615		509-638
AA107515 m	M							14	135			AGC	SKK	1155	364	1	1152	1152		CHR17
AA176563 h, RPSB/C1	H							15	136			AGC	SKK	1410	468	1	1407	1407		12q12-q13.1
AA20680 h, RSK4	H							16	137			AGC	SKK	2738	745	1	2235	2225		Xq21.1
AA215680 h	H							17	138			AGC	SKK	1650	549	1	1647	1647	787-786	14q24.3
SGK h	H							18	139			AGC	SKK	1398	431	1	1293	1293	556-563	6p21-q22
AA107515 m	M							19	140			AGC	SKK	2122	430	75	1364	1290	1804-1830	NA
AA108508 m	M							20	141			AGC	SKK	1346	244	2	733	732		NA
AA887183 h, SGK1, SGK2	H							21	142			AGC	SKK	2250	448	36	1375	1338		NA
AA107883 m	M							22	143			AGC	SKK	1050	349	1	1047	1047		3p14.3
AA172300 h, DRAK2	H							23	144			AGC	AMPK	2310	440	420	1739	1320		1p31.1-p32.3
AA172300 h, DRAK2	H							24	145			AGC	AMPK	3240	682	7	2082	2078	208-227	NA
AA021445 h	H							25	146			AGC	AMPK	1248	297	1	881	881		NA
AA021445 h	H							26	147			AGC	AMPK	2474	668	1	2058	2058	438-458	NA
AA021445 h	H							27	148			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							28	149			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							29	150			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							30	151			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							31	152			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							32	153			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							33	154			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							34	155			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							35	156			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							36	157			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							37	158			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							38	159			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							39	160			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							40	161			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							41	162			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							42	163			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							43	164			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							44	165			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							45	166			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							46	167			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							47	168			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							48	169			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							49	170			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							50	171			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							51	172			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							52	173			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							53	174			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							54	175			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							55	176			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							56	177			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							57	178			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							58	179			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							59	180			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							60	181			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							61	182			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							62	183			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							63	184			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							64	185			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							65	186			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							66	187			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							67	188			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							68	189			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							69	190			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							70	191			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							71	192			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							72	193			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							73	194			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							74	195			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							75	196			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							76	197			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							77	198			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							78	199			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							79	200			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							80	201			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							81	202			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							82	203			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							83	204			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							84	205			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							85	206			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							86	207			AGC	AMPK	2474	668	1	2418	2418		NA
AA021445 h	H							87	208			AGC	AMPK	2474	668	1				



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Table 2

SP	Patent	Seq	Family	Group	nraa	Length	ID	%	Identity	%	nraa	Match	Description	Kinase	Domain(s)	Profile
Seq	ID# aa	Seq	ID# aa	Group	Score	aa	aa	aa	aa	aa	aa	aa	aa	Domain(s)	start	end
H 1	122	AGC	GRK	AGC	2.7e-314	888	887	100	100	100	CAB45857.1	ACCH	BAR2 [Homo sapiens]	191	453	1
M 2	123	AGC	GRK	GRK	1.30E-190	378	371	98	99	99	NP_037029.1	ACCH	Adrenoreceptor kinase, beta 2 (G-protein-linked receptor kinase) [Homo sapiens]	3	143	121
H 3	124	AGC	GRK	GRK	5.80E-108	419	262	71	86	86	CAB76471.1	ACCH	Serine/threonine protein kinase [Homo sapiens]	28	286	1
H 4	125	AGC	GRK	GRK	1.40E-137	414	414	100	100	100	CAB76471.1	ACCH	Serine/threonine protein kinase [Homo sapiens]	23	283	1
H 5	126	AGC	GRK	GRK	1.40E-137	414	414	100	100	100	NP_037386.1	ACCH	TANK-binding kinase 1 [Homo sapiens]	9	304	1
M 6	127	AGC	NDR	NDR	1.20E-09	329	73	46	66	66	BAA76817.1	ACCH	KIAA0973 protein [Homo sapiens]	35	310	1
M 7	128	AGC	NDR	NDR	1.30E-19	88	42	49	71	71	AAF55594.1	ACCH	CG7719 gene product [Drosophila melanogaster]	24	44	242
H 8	129	AGC	NDR	NDR	6.10E-181	464	463	100	100	100	BAA76809.1	ACCH	KIAA0965 protein [Homo sapiens]	90	383	1
H 9	130	AGC	PKC	PKC	8.80E-160	978	815	87	80	80	NP_002733.1	ACCH	Protein kinase C, mu [Homo sapiens]	651	907	1
H 10	131	AGC	PKC	PKC	1.10E-10	105	42	42	57	57	P05127	ACCH	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256
H 11	132	AGC	PKC	PKC	0	890	890	100	100	100	NP_005804.1	ACCH	Protein kinase C, nu [Homo sapiens]	576	832	1
H 12	133	AGC	PKC	PKC	9.4e-319	889	889	100	100	100	NP_037487.1	ACCH	PKNbeta [Homo sapiens]	559	818	1
M 13	134	AGC	PKC	PKC	1.20E-108	205	204	100	100	100	JC7083	ACCH	Protein kinase N beta [Homo sapiens]	1	134	126
H 14	135	AGC	S6K	S6K	3.60E-12	384	94	38	55	55	AAC82495.1	ACCH	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1
H 15	136	AGC	S6K	S6K	2.90E-257	469	489	100	100	100	NP_038556.1	ACCH	Ribosomal protein S6 kinase 3 [Homo sapiens]	225	459	1
H 16	137	AGC	S6K	S6K	7.00E-178	745	745	100	100	100	NP_055311.1	ACCH	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapiens]	73 & 428	330 & 683	1
H 17	138	AGC	S6K	S6K	9.60E-222	549	549	100	100	100	AAD30182.1	ACCH	Unknown [Homo sapiens]	153	539	1
H 18	139	AGC	SGK	SGK	9.20E-103	431	430	100	100	100	AAD41091.1	ACCH	SGK [Homo sapiens]	98	355	1
M 19	140	AGC	SGK	SGK	2.90E-157	430	428	99	99	99	NP_035491.1	ACCH	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1
M 20	141	AGC	SGK	SGK	2.00E-78	244	244	100	100	100	AAF12757.2	ACCH	Protein kinase [Homo sapiens]	162	369	1
H 21	142	AGC	SGK	SGK	4.10E-211	446	375	88	88	88	AAF27051.1	ACCH	SGK-like protein SGK [Homo sapiens]	10	17	253
H 22	143	AGC	SGK	SGK	5.80E-216	349	349	100	100	100	NP_009215.1	ACCH	Protein kinase [Homo sapiens]	40	333	1
H 23	144	AGC	AMPK	AMPK	1.40E-19	440	88	39	61	61	CAAO4119.1	ACCH	Phosphoprotein [Homo sapiens]	368	625	1
H 24	145	AGC	AMPK	AMPK	1.50E-165	699	466	65	77	77	O15075	ACCH	DCAMKL1 (DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1)	59	297	1
M 25	146	AGC	AMPK	AMPK	1.60E-62	297	199	67	83	83	AAF26875.1	ACCH	CPG16 [Mus musculus]	415	673	1
M 26	147	AGC	AMPK	AMPK	2.60E-48	708	181	44	60	60	O15075	ACCH	CPG16 [Mus musculus]	514	771	1
M 28	148	AGC	AMPK	AMPK	2.60E-31	806	147	55	73	73	AAF26875.1	ACCH	CPG16 [Mus musculus]	33	293	1
H 29	149	AGC	AMPK	AMPK	3.10E-121	372	372	100	100	100	NP_004217.1	ACCH	Death-associated protein kinase-related 2	32	293	1
M 30	150	AGC	AMPK	AMPK	7.90E-93	372	340	91	95	95	NP_004217.1	ACCH	Death-associated protein kinase-related 2	32	293	1
H 31	151	AGC	AMPK	AMPK	1.20E-113	414	414	100	100	100	NP_004751.1	ACCH	Death-associated protein kinase-related 1	8	259	1
H 32	152	AGC	AMPK	AMPK	5.80E-165	1311	1053	80	80	80	BAA76843.1	ACCH	KIAA0999 protein [Homo sapiens]	74	325	1
H 33	153	AGC	EMK	EMK	1.20E-45	438	153	51	70	70	T22427	ACCH	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	8	259	1
H 34	154	AGC	EMK	EMK	1.40E-32	438	122	46	65	65	AAC15093.1	ACCH	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	58	307	1
M 35	155	AGC	EMK	EMK	1.30E-184	729	729	100	100	100	AAC15093.1	ACCH	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	59	340	1
H 36	156	AGC	EMK	EMK	3.50E-128	482	482	100	100	100	AAC33487.1	ACCH	R31237, partial CDS [Homo sapiens]	999	1258	1
H 37	157	AGC	EMK	EMK	0	1330	1235	100	100	100	BAA09484.1	ACCH	KIAA0135 gene, related to pim-1 oncogene, [Homo sapiens]	1	158	23
M 38	158	AGC	EMK	EMK	5.10E-59	230	183	79	85	85	BAA09484.1	ACCH	KIAA0135 gene, related to pim-1 oncogene, [Homo sapiens]	20	271	1
H 39	159	AGC	EMK	EMK	3.00E-111	926	636	100	100	100	BAA34501.1	ACCH	KIAA0781 protein [Homo sapiens]	53	304	1
H 40	160	AGC	EMK	EMK	7.30E-80	629	387	57	89	89	NP_055655.1	ACCH	KIAA0537 gene product [Homo sapiens]	81	320	1
H 41	161	AGC	EMK	EMK	1.40E-244	714	714	100	100	100	NP_055401.1	ACCH	Homomally upregulated neu tumor-associated kinase [Homo sapiens]	570	825	1
H 42	162	AGC	EMK	EMK	8.20E-76	874	211	63	80	80	AAAT3168.1	ACCH	Skeletal muscle myosin light chain kinase [Gallus gallus]	820 & 1088	873 & 1358	1
M 43	163	AGC	EMK	EMK	0	2288	2227	100	100	100	BAA92535.1	ACCH	KIAA1297 protein [Homo sapiens]	3	76	186
H 44	164	AGC	EMK	EMK	7.80E-37	127	87	99	99	99	BAA92535.1	ACCH	KIAA1297 protein [Homo sapiens]	985	1239	1
H 45	165	AGC	EMK	EMK	5.00E-20	514	114	41	63	63	NP_008995.1	ACCH	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	116	381	1
H 46	166	AGC	EMK	EMK	3.30E-89	508	181	53	85	85	P25323	ACCH	MLCK [Dicyostelium discoideum]	34	313	1
H 47	167	AGC	EMK	EMK	8.80E-98	478	188	57	88	88	AAF59340.1	ACCH	CG11533 gene product [Drosophila melanogaster]	21	471	1
H 48	168	AGC	EMK	EMK	9.60E-39	286	138	82	79	79	NP_036527.1	ACCH	PFTAIRE protein kinase 1 [Homo sapiens]	1	218	23
H 49	169	AGC	EMK	EMK	7.10E-48	247	146	59	75	75	NP_004187.1	ACCH	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	191	23

Table 2 (cont'd)

M	50	170	CMGC	CDK	2,90E-64	286	193	65	78	NP 004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
M	51	171	CMGC	CDK	1.10E-204	1490	1490	100	100	AAF36401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H	52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF36509.1	NKIATRE [Homo sapiens]	4	385	1	261
M	53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M	54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP 036251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
M	55	175	CMGC	CDK	1.50E-242	499	436	91	93	NP 031740.1	Cell cycle related kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	493	1	261
H	56	176	CMGC	CKL	9.10E-89	544	343	57	64	NP 031740.1	Cell cycle related kinase-like 1 (CDC2-related kinase) [Homo sapiens]	13	305	1	261
H	57	177	CMGC	RCK	2.30E-188	419	419	100	100	NP 055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
M	58	178	CMGC	RCK	1.50E-180	632	632	100	100	NP 055041.1	Renal tumor antigen [Homo sapiens]	4	284	1	261
M	59	179	CMGC	RCK	1.80E-79	413	198	60	77	NP 055041.1	Renal tumor antigen [Homo sapiens]	109	364	1	261
H	60	180	Microbial PK	YGR262.sc	2.50E-45	253	102	46	67	P20689	MLCK [Rattus norvegicus]	101	187	65	147
H	61	181	Other	C28C2.ce	2.30E-158	509	258	100	100	AAF50799.1	CG10673 gene product [Drosophila melanogaster]	2	267	1	261
M	62	182	Other	C28C2.ce	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	88	235	261
H	63	183	Other	C28C2.ce	6.70E-300	1952	1193	99	99	CAB70864.1	Hypothetical protein [Homo sapiens]	221	479	1	261
H	64	184	Other	C28C2.ce	1.10E-254	535	535	100	100	NP 055638.1	KIAA0344 gene product [Homo sapiens]	73	327	1	261
M	65	185	Other	C28C2.ce	2.50E-208	378	372	98	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
M	66	186	Other	C28C2.ce	3.80E-148	588	588	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	165	446	1	261
H	67	187	Other	C28C2.ce	9.90E-24	287	87	33	52	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	24	285	1	261
H	68	188	Other	DYRK	0	1171	1137	97	99	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	199	527	1	261
H	69	189	Other	DYRK	2.10E-280	553	553	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	174	487	1	261
M	70	190	Other	DYRK	2.30E-95	188	149	90	96	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	76	103	235	261
H	71	191	Other	EIFK	0	1649	1493	90	96	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	280 & 590	539 & 1001	1	261
H	72	192	Other	EIFK	1.50E-220	630	630	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	167	583	1	261
M	73	193	Other	Endop	2.50E-45	253	102	46	67	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	101	187	65	147
M	74	194	Other	Endop	3.70E-45	216	100	45	64	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	116	150	116	147
M	75	195	Other	Endop	0	596	596	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	165	443	1	261
M	76	196	Other	IRAK	1.20E-170	392	283	75	85	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	516	777	1	261
H	77	197	Other	IRAK	1.5E-323	922	746	82	88	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	32	318	1	261
H	78	198	Other	KYK2.dd	8.70E-40	225	102	45	62	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	12	266	1	261
H	79	199	Other	KYK2.dd	5.90E-32	280	109	32	50	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	16	259	1	261
M	80	200	Other	LMK	2.80E-17	41	37	92	85	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	463	723	1	261
M	81	201	Other	LMK	2.50E-282	800	799	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	357	620	1	261
H	82	202	Other	MLK	8.80E-251	835	835	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	7	27	181	202
H	83	203	Other	RIP	2.20E-158	634	365	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	57	83	50	78
H	84	204	Other	RIP	5.30E-158	289	288	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	32	327	1	261
M	85	205	Other	SCY1.sc	0	688	688	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	65	131	47	116
H	86	206	Other	SCY1.sc	1.70E-209	505	354	98	98	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	230	305	81	143
H	87	207	Other	SCY1.sc	2.20E-157	808	398	45	61	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	79	531	1	261
H	88	208	Other	SLOB7	7.40E-196	649	649	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	10	265	1	261
H	89	209	Other	SRPK	5.80E-252	533	533	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	25	280	1	261
H	90	210	Other	STK22A	3.80E-53	268	122	46	70	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	12	272	1	261
M	91	211	Other	STK22	2.70E-52	268	127	48	68	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	12	267	1	261
M	92	212	Other	STK22A	4.60E-16	292	112	45	64	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	213	7	261
H	93	213	Other	STK22A	5.10E-123	358	322	90	96	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	329	1	261
H	94	214	Other	TSK	2.10E-33	273	122	46	58	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	80	408	1	261
H	95	215	Other	TSK	0.000082	333	57	36	56	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	8	340	1	261
H	96	216	Other	UNC	0.002492	412	53	37	52	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	57	313	1	261
M	97	217	Other	UNC	0.001096	341	50	36	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	4	285	1	261
H	98	218	Other	UNC	1.90E-68	480	247	100	100	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	39	84	124
H	99	219	Other	UNC	1.60E-208	565	468	96	96	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	39	84	124
H	100	220	Other	UNC	8.70E-10	39	27	69	90	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	39	84	124
H	101	221	Other	UNC	8.70E-10	39	27	69	90	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	39	84	124
H	102	222	Other	UNC	8.70E-10	39	27	69	90	NP 037524.1	Nuclear receptor binding protein [Homo sapiens]	1	39	84	124



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Table 2 (cont'd)

M	103	222	Other	Unque	0.000022	349	38	30	50	CAA18118.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H	104	223	Other	Unque	0.000128	704	54	30	45	BAA86578.1	KIAA1284 protein [Homo sapiens]	1	246	25	261
M	105	224	Other	Unque	0.007385	540	25	42	61	AAF47918.1	Tie gene product [Drosophila melanogaster]	9	104	168	261
H	106	225	Other	Unque	0.31334	540	52	30	42	P10162	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M	107	226	Other	Unque	0.022848	365	25	34	57	NP_006276.1	Testis-specific kinase 1 [Homo sapiens]	68	96	42	71
H	108	227	Other	VRK	3.10E-263	474	474	100	100	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M	109	228	Other	VRK	1.20E-111	234	191	82	90	BAA90769.1	Vaccinia related kinase 3 [Homo sapiens]	7	78	63	136
H	110	229	Other	YPL236.sc	7.40E-144	305	304	100	100	AAC28337.1	MPSK [Homo sapiens]	20	290	1	261
H	111	230	Other	YQ09.ce	5.10E-49	581	135	43	83	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H	112	231	STE	NEK	3.30E-30	898	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H	113	232	STE	NEK	2.70E-119	838	357	88	86	AAD31939.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H	114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004683.1	mitogen-activated protein kinase kinase kinase 8 [Homo sapiens]	376	629	6	261
H	115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA94194.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H	116	235	TK	RTK-20	4.90E-24	495	77	38	56	AAA98465.1	(U00827) protein tyrosine kinase [Mus musculus]	187	453	1	261
M	117	236	TK	RTK-20	5.30E-18	183	53	38	57	NP_032036.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H	118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H	120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	267	1	261
H	121	239	Other	LINK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

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Table 3

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Tissue	Tumor-seq	Normal-seq	Tumor - 1a	Tumor cells	Normal	Endom	p33	SEQ 003	AMEG 5	TBM	SEQ 006	AMEG 8	AMEG 9	CAESG 11	EMSG 12	PMSE 14	MTSE 16	18		
adipose - h	2							7490	13681	501221	29441	34705	56943	11808	46620	12165				
adipose - h	2							8151	32265	1202494	118257	105718	55339	19907	94529	14258				
adipose - h	2							4445	9326	1477546	35347	32227	33560	13151	22524	12409				
adipose - h	2							964	376	109987	4021	4318	1984	1985	24739	2903				
adipose - h	2							9649	5023	239783	62822	21880	7861	7736	34253	7107				
adipose - h	2							5423	3574	334665	50825	32290	8621	11895	62536	13345				
adipose - h	2							6350	19704	787223	84608	35492	16370	28260	82536	12780				
adipose - h	2							8342	7684	125184	80457	34563	18473	11010	87365	12180				
adipose - h	2							15119	6044	967041	80401	30156	23343	13781	103271	8901				
adipose - h	2							8763	15450	1232178	46305	43070	24271	13687	80242	10901				
adipose - h	2							4107	10639	337527	51069	87948	31171	19966	65084	10989				
adipose - h	2							11	1784	122058	82025	48912	11790	9484	74734	11184				
adipose - h	2							12	5294	1548111	38106	35129	17029	10418	68677	14403				
adipose - h	2							13	3698	429781	37947	37750	11433	13006	82783	8440				
adipose - h	2							14	8451	1305467	79618	12219	10828	11874	57531	8265				
adipose - h	2							15	5185	2736	224006	21860	24702	7820	8406	48325	12082			
adipose - h	2							16	3012	1915	227834	27479	20872	6357	11717	43891	11051			
adipose - h	2							17	3020	5561	533116	28567	28503	11720	12220	4844	54755	8768		
adipose - h	2							18	3568	3455	412001	41491	24702	7820	8406	48325	12082			
adipose - h	2							19	3183	4479	303667	34663	16281	11656	6363	40333	8303			
adipose - h	2							20	3364	1519	206005	46111	29975	10830	4418	37827	7084			
adipose - h	2							21	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							22	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							23	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							24	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							25	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							26	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							27	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							28	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							29	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							30	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							31	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							32	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							33	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							34	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							35	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							36	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							37	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							38	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							39	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							40	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							41	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							42	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							43	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							44	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							45	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							46	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							47	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							48	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							49	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							50	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							51	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							52	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							53	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							54	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							55	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							56	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							57	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							58	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							59	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							60	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							61	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							62	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							63	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							64	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							65	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							66	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							67	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							68	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							69	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							70	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							71	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							72	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							73	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							74	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							75	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							76	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							77	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							78	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							79	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							80	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							81	4121	1821	448677	25131	26347	7820	8406	48325	12082			
adipose - h	2							82	4											

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Table 3 (cont'd)[illegible]

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Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor site	Tumor side	Normal	Endoc	p53	SEC 003	AMEQ 3	TAB-SEQ	004	AMEQ 3	005	AMEQ 3	CAR-SEQ	11	EP-SEQ	12	PM-SEQ	14	MEQ	16	R
DuPang-7								4091	4152	130751	48007	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-8								1843	0	129284	31586	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-9								1704	352	21317	22363	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-11								2364	2910	36636	34352	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-12								1821	0	143418	14784	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-10								1137	11437	58718	25013	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-1								1808	0	176875	87121	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-2								778	282	80117	44121	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-3								1030	5099	98419	23123	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-4								44	3575	48050	18490	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-5								447	217	37704	9958	0	0	0	0	0	0	0	0	0	0	0	0
DuPang-6								1734	0	104257	34586	0	0	0	0	0	0	0	0	0	0	0	0
AS49-8								1411	1853	30554	11740	0	0	0	0	0	0	0	0	0	0	0	0
SKVX-8								mutant	2911	8405	74732	34175	0	0	0	0	0	0	0	0	0	0	0
SV-208-7								wt	458	0	48374	18406	0	0	0	0	0	0	0	0	0	0	0
MCT-118-7								wt	360	846	69043	25676	0	0	0	0	0	0	0	0	0	0	0
MCT-118-8								mutant	290	3501	23154	10610	0	0	0	0	0	0	0	0	0	0	0
HT29-1								mutant	78	3147	8867	8481	0	0	0	0	0	0	0	0	0	0	0
HT29-7								mutant	181	467	50732	18019	0	0	0	0	0	0	0	0	0	0	0
HT29-8								wt	7388	375	15255	8177	0	0	0	0	0	0	0	0	0	0	0
SPF39-7								wt	0	0	57878	8736	0	0	0	0	0	0	0	0	0	0	0
SPF39-8								mutant	507	448	33057	13175	0	0	0	0	0	0	0	0	0	0	0
SPF39-9								mutant	802	0	30102	6841	0	0	0	0	0	0	0	0	0	0	0
SV-208-8								wt	661	1295	72107	15662	0	0	0	0	0	0	0	0	0	0	0
OVCAR-4-7								wt	1380	527	105548	21701	0	0	0	0	0	0	0	0	0	0	0
OVCAR-4-8								mutant	0	338	32948	10750	0	0	0	0	0	0	0	0	0	0	0
OVCAR-5-7								wt	152	0	12818	10657	0	0	0	0	0	0	0	0	0	0	0
OVCAR-5-8								mutant	555	740	24190	11853	0	0	0	0	0	0	0	0	0	0	0
MCF-7-8								mutant	832	3013	12554	17722	0	0	0	0	0	0	0	0	0	0	0
ADR-RES-8								HPV E6	0	2243	23853	106	0	0	0	0	0	0	0	0	0	0	0
HsL-8								mutant	727	1081	24521	12011	0	0	0	0	0	0	0	0	0	0	0
SW480-7								mutant	226	7328	43102	8409	0	0	0	0	0	0	0	0	0	0	0
SW480-8								mutant	192	2383	53893	10761	0	0	0	0	0	0	0	0	0	0	0
HT29-8								mutant	372	3129	11402	2174	0	0	0	0	0	0	0	0	0	0	0
C3A-7								mutant	0	18121	30317	18670	0	0	0	0	0	0	0	0	0	0	0
C3A-8								mutant	20	2184	72622	14777	0	0	0	0	0	0	0	0	0	0	0
UZOS-7								mutant	87	0	156967	6029	0	0	0	0	0	0	0	0	0	0	0
UZOS-8								wt	539	4926	29729	12066	0	0	0	0	0	0	0	0	0	0	0
HsL-7								wt	302	4487	24757	14258	0	0	0	0	0	0	0	0	0	0	0
HsL-8								wt	232	87	9236	7519	0	0	0	0	0	0	0	0	0	0	0
WT38-8								wt	8548	0	615446	28622	15378	21529	3328	37566	7008						
hsc-mycRNA								0	110	0	1153	687	28811	1237	25544	2086							
KPL1572 3/17/89								0	348	1576	68918	7421	4939	12083	23363	59610	5229						
Bea-4								1340	505	87915	9787	4804	8547	918	5255	7646							
HT29-8								197	345	18828	8158	4064	4910	728	37558	5769							
HT29-8								2178	0	88268	34038	7565	18311	2626	78412	7537							
HT29-8								0	390	86196	8634	704	7098	2008	21762	8907							
Bea-3								173	40	808	9532	3342	193	2825	705	38421	2784						
Bea-3								177	325	0	8094	1215	1068	663	751	19950	1629						
Bea-8								1003	0	14485	12819	1856	1118	1962	35076	4236							
hsc-mycRNA 2/25/92 #10								881	0	52581	8298	1547	8229	2251	52527	6863							
Bea-10								138	0	18813	8510	5486	15018	1115	86289	14731							
HTB10								515	0	77283	9059	253	3034	1099	43314	8186							
hsc-mycRNA 3/3/92 #12								384	37	2733	5219	1565	5617	34	28033	5417							
pcna10								486	0	280879	11883	2184	10484	1829	24878	4588							
MANK-OS poly A*								1201	0	28774	11088	2632	1806	1555	27087	4278							
SA-OS (Mamory) poly A*								1882	354	75322	17889	3824	3418	2424	32134	7106							
hsc-poly A*								wt	420	2054	86454	8649	0	0	0	0	0						
MCT-118-7								wt	587	0	59778	8562	0	0	0	0	0						
MCT-118-4								wt	258	377	34535	13003	0	0	0	0	0						
MCT-118-5								wt	0	249	83380	12796	0	0	0	0	0						
MCT-118-6								wt	0	43489	3320	0	0	0	0	0	0						
AS49-8								mutant	302	3771	40884	8815	0	0	0	0	0						
HT29-3								mutant	238	0	82983	8837	0	0	0	0	0						
SKVX-8								mutant	27	0	88030	8240	0	0	0	0	0						
HT29-4								mutant	445	1208	25013	18178	0	0	0	0	0						
HT29-8								mutant	309	0	54935	10000	0	0	0	0	0						
HT29-8								wt	581	1208	50523	11477	0	0	0	0	0						
OVCAR-3								wt	225	487	63478	8801	0	0	0	0	0						
OVCAR-4-4								wt	45	2526	84029	14924	0	0	0	0	0						
OVCAR-4-5								wt	0	522	28881	8741	0	0	0	0	0						
OVCAR-4-8								wt	301	0	53862	12881	0	0	0	0	0						
SPF39-3								wt	403	0	34234	15917	0	0	0	0	0						
SPF39-4								wt	263	1459	18387	12742	0	0	0	0	0						
SPF39-5								wt	0	817	27987	14894	0	0	0	0	0						
SPF39-6								mutant	648	2513	51462	8772	0	0	0	0	0						
OVCAR-5-3								wt	0	3066	14548	10469	0	0	0	0	0						
OVCAR-5-4								mutant	512	444	8783	7292	0	0	0	0	0						
OVCAR-5-6								mutant	215	992	19534	7377	0	0	0	0	0						
ADR-RES-8								wt	711	2112	80711	12218	0	0	0	0	0						
MCF-7-8								HPV E6	0	0	52580	16708	0	0	0	0	0						
HsL-8								mutant	313	358													

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Table 3 (cont'd)[illegible]

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Table 3 (cont'd)

Transcript	Turnon-5'ym	Normal-5'ym	Turnon - 10	Turnon 5'ym	Normal	Endon	p33	5' SEQ 17	ANSEQ 20	SGSEQ 22	PTTSEQ 23	ANSEQ 25	DNSEQ 31	DNSEQ 32	ANSEQ 45	M4 SEQ 84	T
7B-1	166		166					25441	0	0	777	871	4112	0	0	0	
7B-2	189		189					43353	+15	10 64	2482	2283	8374	109	0	0	
7B-3	189		189					43353	0	44 22	838	77	1518	1109	0	0	129
7B-4	171		171					20043	0	41	218	500	0	0	0	0	81
7B-5	183		183					11552	0	486	1671	242	339	32	197	178	
7B-6	183		183					21215	0	0	0	0	0	691	120	0	
7B-7	23562	194	0	1630	2050	1064	265	0	0	0	0	0	0	0	0	0	
7B-8	20104	0	0	1156	1462	145	462	0	0	0	0	0	0	0	0	0	
7B-9	23610	0	1874	1096	523	874	750	371	129	0	0	0	0	0	0	0	
7B-10	200	19130	130	99	1294	812	848	0	0	0	0	0	0	0	0	0	
7B-11	2081	314	0	78	495	213	178	0	0	0	0	0	0	0	0	0	
7B-12	8406	0	24	1294	572	149	0	0	0	0	0	0	0	0	0	0	
7B-13	2080	0	0	14	0	82	0	0	0	0	0	0	0	0	0	0	
7B-14	83548	0	1041	3506	14092	911	411	0	0	0	0	0	0	0	0	0	
7B-15	218	0	0	621	47	0	0	0	0	0	0	0	0	0	0	0	
7B-16	20009	0	0	0	2727	0	149	178	134	0	0	0	0	0	0	0	
7B-17	14725	0	133	0	0	355	862	0	0	0	0	0	0	0	0	0	
7B-18	20116	84	0	1488	338	487	157	361	0	0	0	0	0	0	0	0	
7B-19	32466	263	0	0	0	235	0	0	0	0	0	0	0	0	0	0	
7B-20	37536	43	804	154	0	22	0	0	0	0	0	0	0	0	0	0	
7B-21	22249	0	0	0	0	706	740	63	0	0	0	0	0	0	0	0	
7B-22	18708	0	143	1383	0	24	204	836	0	0	0	0	0	0	0	0	
7B-23	22457	347	303	1606	537	2757	371	0	0	0	0	0	0	0	0	0	
7B-24	33149	0	0	0	0	4253	2803	0	0	0	0	0	0	0	0	0	
7B-25	20642	860	901	268	307	1098	1118	1184	14	0	0	0	0	0	0	0	
7B-26	34473	0	0	29	567	1812	244	2675	26	0	0	0	0	0	0	0	
7B-27	34516	0	0	685	0	0	153	812	401	0	0	0	0	0	0	0	
7B-28	19586	0	1251	0	354	730	0	897	62	0	0	0	0	0	0	0	
7B-29	37443	309	200	689	893	1417	264	2675	26	0	0	0	0	0	0	0	
7B-30	34819	0	5778	813	1804	2385	1674	204	0	0	0	0	0	0	0	0	
7B-31	10333	4781	1977	0	157	587	0	718									

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Table 3 (cont'd)

Team	Tumor - 3m	Normal - 3m	Tumor - 1g	Tumor - 2g	Normal	Endo	32	50	64	128	256	512	1024	2048	4096	8192	16384	32768	65536	131072	262144	524288	1048576	2097152	4194304	8388608	16777216	33554432	67108864	134217728	268435456	536870912	1073741824	2147483648	4294967296	8589934592	17179869184	34359738368	68719476736	137438953472	274877906944	549755813888	1099511627776	2199023255552	4398046511104	8796093022208	17592186044416	35184372088832	70368744177664	140737488355328	281474976710656	562949953421312	1125899906842624	2251799813685248	4503599627370496	9007199254740992	18014398509481984	36028797018963968	72057594037927936	144115188075855872	288230376151711744	576460752303423488	1152921504606846976	2305843009213693952	4611686018427387904	9223372036854775808	18446744073709551616	36893488147419103232	73786976294838206464	147573952589676412928	295147905179352825856	590295810358705651712	1180591620717411303424	2361183241434822606848	4722366482869645213696	9444732965739290427392	18889465931478580854784	37778931862957161709568	75557863725914323419136	151115727451828646838272	302231454903657293676544	604462909807314587353088	1208925819614629174706176	2417851639229258349412352	4835703278458516698824704	9671406556917033397649408	19342813113834066795298816	38685626227668133590597632	77371252455336267181195264	154742504910672534362390528	309485009821345068724781056	618970019642690137449562112	1237940039285380274899124224	2475880078570760549798248448	4951760157141521099596496896	9903520314283042199193993792	19807040628566084398387987584	39614081257132168796775975168	79228162514264337593551950336	158456325028528675187103900672	316912650057057350374207801344	633825300114114700748415602688	1267650600228229401496831205376	2535301200456458802993662410752	5070602400912917605987324821504	10141204801825835211974649643008	20282409603651670423949299286016	40564819207303340847898598572032	81129638414606681695797197144064	162259276829213363391594394288128	324518553658426726783188788576256	649037107316853453566377577152512	1298074214633706907132755154305024	2596148429267413814265510308610048	519229685853482762853102061722016	1038459371706965525706204123444032	2076918743413931051412408246888064	4153837486827862102824816493776128	8307674973635724205649632987552256	16615349947271448411299265975104512	332306998945428968225985319502081024	664613997890857936451970639004162048	1329227995781715873835941278008324096	2658455991563431747671882556016648192	53169119831268634953437651120328963384	106338239662537269866875302240657966768	212676479325074539733750604481315933536	425352958650149079467501208962628667104	850705917300298158935002417925253334208	1701411834600596317870004835850506668416	3402823669201192635740009671701013336832	6805647338402385271480001943402026673664	13611294676804770542960003886804053347328	27222589353609541085920007773608106694656	54445178707219082171840001554721621338912	108890357414438164343680003109442442677824	217780714828876328687360006218884885355456	4355614296577526573747200012377777071111104	8711228593155053147494400024755554042222208	17422451986310106294988800049511118084444416	3484490397262021258997760009902223616888832	69689807945240425179955200019804472337777664	13937961589048085035991040003960894467555528	27875923178096170071982080007921788931111156	55751846356192340143964160001584357782222312	11150369271238468287992832000316871554
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Table 3 (cont'd)

[illegible]



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Table 3 (cont'd)

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Table 3 (cont'd)

Tissue	Tumor-dyn	Normal-dyn	Tumor - fa	Tumor cells	Normal	Endos	p33	SEQ 17	AA	SEQ 20	SG	SEQ 22	PT	SEQ 24	AA	SEQ 25	DR	SEQ 31	DR	SEQ 32	AA	SEQ 40	MA	SEQ 44	T	
DuPang-7								0	0	0	0	0	0	2184	1	8478	31596	2728	1224	0					0	
DuPang-8								0	0	0	0	0	0	1005	1	17454	14890	1078	0						0	
DuPang-11								0	0	0	0	0	0	9122	1	1508	25973	1316	62						0	
DuPang-12								0	0	0	0	0	0	7501	1	8216	14351	1857	968						0	
DuPang-10								0	0	0	0	0	0	3497	1	3256	16748	1020	0						0	
DuPang-1								0	0	0	0	0	0	6442	1	298	12428	3111	210						0	
DuPang-2								0	0	0	0	0	0	3941	1	12536	8767	832	17852						0	
DuPang-3								0	0	0	0	0	0	3679	1	10380	6377	148	69625						0	
DuPang-5								0	0	0	0	0	0	1744	1	2846	2782	3207	4773						0	
DuPang-6								0	0	0	0	0	0	1944	1	4731	87	4214	593						0	
A549 - 6								0	0	0	0	0	0	1170	1	2028	327	1817	2163						0	
EXVX - 6								0	0	0	0	0	0	12027	1	5346	0	2630	1433						0	
HCT-116 - 7								0	0	0	0	0	0	1464	1	8852	0	427	0						0	
HCT-116 - 8								0	0	0	0	0	0	1513	1	2153	6498	580	0						0	
HT29 - 1								0	0	0	0	0	0	742	1	2507	3043	5490	619						0	
HT29 - 7								0	0	0	0	0	0	814	1	5117	2307	781	0						0	
HT29 - 8								0	0	0	0	0	0	420	1	3056	3122	801	0						0	
SF539 - 7								0	0	0	0	0	0	444	1	150	0	0	0						0	
SF539 - 8								0	0	0	0	0	0	1051	1	2906	2178	0	1148						0	
SF-205-7								0	0	0	0	0	0	1143	1	2853	2927	562	0						0	
SF-205-8								0	0	0	0	0	0	86	1	10246	2863	1075	208						0	
OVCA8-4 - 7								0	0	0	0	0	0	771	1	8991	2712	1158	1054						0	
OVCA8-4 - 8								0	0	0	0	0	0	1180	1	8734	4422	384	0						0	
OVCA8-5 - 7								0	0	0	0	0	0	0	1284	1	6063	0	0						0	
OVCA8-5 - 8								0	0	0	0	0	0	2050	1	2109	13609	585	3738						0	
AMC7-7 - 8								0	0	0	0	0	0	89	1	957	21830	0	0						0	
ADR-RES - 6								0	0	0	0	0	0	2453	1	7100	2592	0	0						0	
HsA - 6								0	0	0	0	0	0	2530	1	1521	0	0	1907						0	
SW480 - 7								0	0	0	0	0	0	465	1	672	3321	0	0						0	
SW480 - 8								0	0	0	0	0	0	1828	1	225	4795	1418	0						0	
HT29 - 8								0	0	0	0	0	0	248	1	841	4942	0	0						0	
C33A - 7								0	0	0	0	0	0	0	870	1	4326	0	1186						0	
C33A - 8								0	0	0	0	0	0	1405	1	4781	2485	208	48						0	
U2OS - 7								0	0	0	0	0	0	0	2552	1	2718	1002	837						0	
U2OS - 8								0	0	0	0	0	0	0	5663	1	805	0	0						0	
HsA - 7								0	0	0	0	0	0	2235	1	4848	3016	877	1215						0	
HsA - 8								0	0	0	0	0	0	4460	1	461	805	0	0						0	
WI 38 - 8								0	0	0	0	0	0	1026	1	348	8018	0	0						0	
158 multiple RNA								0	0	0	0	0	0	1448	1	1163	3374	1862	0						0	
CIN 1572 317789								0	0	0	0	0	0	1470	1	0	3574	0	455	0						0
Bea								37888	0	4415	0	0	0	215	1	299	1447	8183	0						0	
HT29-8								25564	878	738	643	4685	0	27	1	578	18	0	0						0	
HT29-8								32584	0	0	1007	3021	1552	0	1	236	0	0							0	
HT29-8								7527	0	0	7527	21100	3372	29	0	301	0	0							0	
HT29-8								37556	8	308	862	2880	5814	0	1	0	0	0							0	
Bea-3								21782	851	0	14370	8958	1350	316	0	0	0	0							0	
Bea-5								38821	38	0	0	32209	1163	165	873	574	0	0							0	
Bea-8								173	173	0	0	1854	1010	76	178	0	0	0							0	
h human myocyt 275/22 #10								177	177	0	0	0	311	0	0	0	0	0							0	
Bea-10								60327	0	142	393	0	643	0	0	0	0	0							0	
HT29-10								237	237	0	3049	664	48	0	0	0	0	0							0	
h fibroblast 3/21/02 #12								45182	287	0	245	732	2284	0	0	0	0	0							0	
prostate h								44371	0	0	1379	3583	0	0	0	0	0	0							0	
hHNSC-C5 poly A+								88	88	0	0	4810	70	0	0	0	0	0							0	
SA-C6 (Rumby) poly A+								28035	7	0	0	5762	14	0	0	0	0	0							0	
hH poly A+								24878	236	1075	3582	3701	1721	1048	0	0	0	0							0	
HCT-116 - 3								27881	0	0	10786	9841	874	0	0	0	0	0							0	
HCT-116 - 4								32124	0	281	12028	10417	472	1862	0	0	0	0							0	
HCT-116 - 5								0	0	0	11	1788	4464	227	0	0	0	0							0	
HCT-116 - 6								0	0	0	0	3318	7970	113	0	0	0	0							0	
A549 - 5								0	0	0	1789	1899	3247	0	0	0	0	0							0	
HT29 - 3								0	0	0	0	7818	287	245	0	0	0	0							0	
EXVX - 6								0	0	0	0	2201	62	0	0	0	0	0							0	
HT29 - 4								0	0	0	0	14	6524	7475	1143	513	0	0							0	
HT29 - 5								0	0	0	0	1948	2378	0	429	0	0	0							0	
HT29 - 6								0	0	0	0	1238	333	3234	181	0	0	0							0	
OVCA8-4 - 3								0	0	0	0	1070	3806	3867	0	363	0	0							0	
OVCA8-4 - 4								0	0	0	0	0	3905	5470	870	3059	0	0							0	
OVCA8-4 - 5								0	0	0	0	1203	1813	11856	870	0	0	0							0	
OVCA8-4 - 6								0	0	0	0	0	708	8723	708	689	0	0							0	
SF539 - 3								0	0	0	0	859	3034	2676	211	0	0	0							0	
SF539 - 4								0	0	0	0	813	10679	13756	1759	3849	0	0							0	
SF539 - 5								0	0	0	0	1208	4103	1672	150	286	0	0							0	
SF539 - 6								0	0	0	0	0	1893	2256	414	109	0	0							0	
OVCA8-5 - 3								0	0	0	0	886	1252	2280	414	0	0	0							0	
OVCA8-5 - 4								0	0	0	0	1847	8497	7120	0	111	0	0							0	
OVCA8-5 - 5								0	0	0	0	236	3700	2418	281	400	0	0							0	
ADR-RES - 6								0	0	0	0	348	1853	13	0	0	0	0							0	
AMC7-7 - 8								0	0</																	



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Table 3 (cont'd)

Tissue	Tumor type	Normal	Tumor - 1a	Tumor cells	Normal	Endoth	32	SEG 8a	TSEG 45	AMSEG 47	AMSEG 48	AMSEG 49	AMSEG 50	AMSEG 51	AMSEG 52	AMSEG 53	AMSEG 54	AMSEG 55	AMSEG 56	AMSEG 57	AMSEG 58	AMSEG 59	AMSEG 60	AMSEG 61	AMSEG 62	AMSEG 63	AMSEG 64	AMSEG 65	AMSEG 66	AMSEG 67	AMSEG 68	AMSEG 69	AMSEG 70	AMSEG 71	AMSEG 72	AMSEG 73	AMSEG 74	AMSEG 75	AMSEG 76	AMSEG 77	AMSEG 78	AMSEG 79	AMSEG 80	AMSEG 81	AMSEG 82	AMSEG 83	AMSEG 84	AMSEG 85	AMSEG 86	AMSEG 87	AMSEG 88	AMSEG 89	AMSEG 90	AMSEG 91	AMSEG 92	AMSEG 93	AMSEG 94	AMSEG 95	AMSEG 96	AMSEG 97	AMSEG 98	AMSEG 99	AMSEG 100	AMSEG 101	AMSEG 102	AMSEG 103	AMSEG 104	AMSEG 105	AMSEG 106	AMSEG 107	AMSEG 108	AMSEG 109	AMSEG 110	AMSEG 111	AMSEG 112	AMSEG 113	AMSEG 114	AMSEG 115	AMSEG 116	AMSEG 117	AMSEG 118	AMSEG 119	AMSEG 120	AMSEG 121	AMSEG 122	AMSEG 123	AMSEG 124	AMSEG 125	AMSEG 126	AMSEG 127	AMSEG 128	AMSEG 129	AMSEG 130	AMSEG 131	AMSEG 132	AMSEG 133	AMSEG 134	AMSEG 135	AMSEG 136	AMSEG 137	AMSEG 138	AMSEG 139	AMSEG 140	AMSEG 141	AMSEG 142	AMSEG 143	AMSEG 144	AMSEG 145	AMSEG 146	AMSEG 147	AMSEG 148	AMSEG 149	AMSEG 150	AMSEG 151	AMSEG 152	AMSEG 153	AMSEG 154	AMSEG 155	AMSEG 156	AMSEG 157	AMSEG 158	AMSEG 159	AMSEG 160	AMSEG 161	AMSEG 162	AMSEG 163	AMSEG 164	AMSEG 165	AMSEG 166	AMSEG 167	AMSEG 168	AMSEG 169	AMSEG 170	AMSEG 171	AMSEG 172	AMSEG 173	AMSEG 174	AMSEG 175	AMSEG 176	AMSEG 177	AMSEG 178	AMSEG 179	AMSEG 180	AMSEG 181	AMSEG 182	AMSEG 183	AMSEG 184	AMSEG 185	AMSEG 186	AMSEG 187	AMSEG 188	AMSEG 189	AMSEG 190	AMSEG 191	AMSEG 192	AMSEG 193	AMSEG 194	AMSEG 195	AMSEG 196	AMSEG 197	AMSEG 198	AMSEG 199	AMSEG 200	AMSEG 201	AMSEG 202	AMSEG 203	AMSEG 204	AMSEG 205	AMSEG 206	AMSEG 207	AMSEG 208	AMSEG 209	AMSEG 210	AMSEG 211	AMSEG 212	AMSEG 213	AMSEG 214	AMSEG 215	AMSEG 216	AMSEG 217	AMSEG 218	AMSEG 219	AMSEG 220	AMSEG 221	AMSEG 222	AMSEG 223	AMSEG 224	AMSEG 225	AMSEG 226	AMSEG 227	AMSEG 228	AMSEG 229	AMSEG 230	AMSEG 231	AMSEG 232	AMSEG 233	AMSEG 234	AMSEG 235	AMSEG 236	AMSEG 237	AMSEG 238	AMSEG 239	AMSEG 240	AMSEG 241	AMSEG 242	AMSEG 243	AMSEG 244	AMSEG 245	AMSEG 246	AMSEG 247	AMSEG 248	AMSEG 249	AMSEG 250	AMSEG 251	AMSEG 252	AMSEG 253	AMSEG 254	AMSEG 255	AMSEG 256	AMSEG 257	AMSEG 258	AMSEG 259	AMSEG 260	AMSEG 261	AMSEG 262	AMSEG 263	AMSEG 264	AMSEG 265	AMSEG 266	AMSEG 267	AMSEG 268	AMSEG 269	AMSEG 270	AMSEG 271	AMSEG 272	AMSEG 273	AMSEG 274	AMSEG 275	AMSEG 276	AMSEG 277	AMSEG 278	AMSEG 279	AMSEG 280	AMSEG 281	AMSEG 282	AMSEG 283	AMSEG 284	AMSEG 285	AMSEG 286	AMSEG 287	AMSEG 288	AMSEG 289	AMSEG 290	AMSEG 291	AMSEG 292	AMSEG 293	AMSEG 294	AMSEG 295	AMSEG 296	AMSEG 297	AMSEG 298	AMSEG 299	AMSEG 300	AMSEG 301	AMSEG 302	AMSEG 303	AMSEG 304	AMSEG 305	AMSEG 306	AMSEG 307	AMSEG 308	AMSEG 309	AMSEG 310	AMSEG 311	AMSEG 312	AMSEG 313	AMSEG 314	AMSEG 315	AMSEG 316	AMSEG 317	AMSEG 318	AMSEG 319	AMSEG 320	AMSEG 321	AMSEG 322	AMSEG 323	AMSEG 324	AMSEG 325	AMSEG 326	AMSEG 327	AMSEG 328	AMSEG 329	AMSEG 330	AMSEG 331	AMSEG 332	AMSEG 333	AMSEG 334	AMSEG 335	AMSEG 336	AMSEG 337	AMSEG 338	AMSEG 339	AMSEG 340	AMSEG 341	AMSEG 342	AMSEG 343	AMSEG 344	AMSEG 345	AMSEG 346	AMSEG 347	AMSEG 348	AMSEG 349	AMSEG 350	AMSEG 351	AMSEG 352	AMSEG 353	AMSEG 354	AMSEG 355	AMSEG 356	AMSEG 357	AMSEG 358	AMSEG 359	AMSEG 360	AMSEG 361	AMSEG 362	AMSEG 363	AMSEG 364	AMSEG 365	AMSEG 366	AMSEG 367	AMSEG 368	AMSEG 369	AMSEG 370	AMSEG 371	AMSEG 372	AMSEG 373	AMSEG 374	AMSEG 375	AMSEG 376	AMSEG 377	AMSEG 378	AMSEG 379	AMSEG 380	AMSEG 381	AMSEG 382	AMSEG 383	AMSEG 384	AMSEG 385	AMSEG 386	AMSEG 387	AMSEG 388	AMSEG 389	AMSEG 390	AMSEG 391	AMSEG 392	AMSEG 393	AMSEG 394	AMSEG 395	AMSEG 396	AMSEG 397	AMSEG 398	AMSEG 399	AMSEG 400	AMSEG 401	AMSEG 402	AMSEG 403	AMSEG 404	AMSEG 405	AMSEG 406	AMSEG 407	AMSEG 408	AMSEG 409	AMSEG 410	AMSEG 411	AMSEG 412	AMSEG 413	AMSEG 414	AMSEG 415	AMSEG 416	AMSEG 417	AMSEG 418	AMSEG 419	AMSEG 420	AMSEG 421	AMSEG 422	AMSEG 423	AMSEG 424	AMSEG 425	AMSEG 426	AMSEG 427	AMSEG 428	AMSEG 429	AMSEG 430	AMSEG 431	AMSEG 432	AMSEG 433	AMSEG 434	AMSEG 435	AMSEG 436	AMSEG 437	AMSEG 438	AMSEG 439	AMSEG 440	AMSEG 441	AMSEG 442	AMSEG 443	AMSEG 444	AMSEG 445	AMSEG 446	AMSEG 447	AMSEG 448	AMSEG 449	AMSEG 450	AMSEG 451	AMSEG 452	AMSEG 453	AMSEG 454	AMSEG 455	AMSEG 456	AMSEG 457	AMSEG 458	AMSEG 459	AMSEG 460	AMSEG 461	AMSEG 462	AMSEG 463	AMSEG 464	AMSEG 465	AMSEG 466	AMSEG 467	AMSEG 468	AMSEG 469	AMSEG 470	AMSEG 471	AMSEG 472	AMSEG 473	AMSEG 474	AMSEG 475	AMSEG 476	AMSEG 477	AMSEG 478	AMSEG 479	AMSEG 480	AMSEG 481	AMSEG 482	AMSEG 483	AMSEG 484	AMSEG 485	AMSEG 486	AMSEG 487	AMSEG 488	AMSEG 489	AMSEG 490	AMSEG 491	AMSEG 492	AMSEG 493	AMSEG 494	AMSEG 495	AMSEG 496	AMSEG 497	AMSEG 498	AMSEG 499	AMSEG 500	AMSEG 501	AMSEG 502	AMSEG 503	AMSEG 504	AMSEG 505	AMSEG 506	AMSEG 507	AMSEG 508	AMSEG 509	AMSEG 510	AMSEG 511	AMSEG 512	AMSEG 513	AMSEG 514	AMSEG 515	AMSEG 516	AMSEG 517	AMSEG 518	AMSEG 519	AMSEG 520	AMSEG 521	AMSEG 522	AMSEG 523	AMSEG 524	AMSEG 525	AMSEG 526	AMSEG 527	AMSEG 528	AMSEG 529	AMSEG 530	AMSEG 531	AMSEG 532	AMSEG 533	AMSEG 534	AMSEG 535	AMSEG 536	AMSEG 537	AMSEG 538	AMSEG 539	AMSEG 540	AMSEG 541	AMSEG 542	AMSEG 543	AMSEG 544	AMSEG 545	AMSEG 546	AMSEG 547	AMSEG 548	AMSEG 549	AMSEG 550	AMSEG 551	AMSEG 552	AMSEG 553	AMSEG 554	AMSEG 555	AMSEG 556	AMSEG 557	AMSEG 558	AMSEG 559	AMSEG 560	AMSEG 561	AMSEG 562	AMSEG 563	AMSEG 564	AMSEG 565	AMSEG 566	AMSEG 567	AMSEG 568	AMSEG 569	AMSEG 570	AMSEG 571	AMSEG 572	AMSEG 573	AMSEG 574	AMSEG 575	AMSEG 576	AMSEG 577	AMSEG 578	AMSEG 579	AMSEG 580	AMSEG 581	AMSEG 582	AMSEG 583	AMSEG 584	AMSEG 585	AMSEG 586	AMSEG 587	AMSEG 588	AMSEG 589	AMSEG 590	AMSEG 591	AMSEG 592	AMSEG 593	AMSEG 594	AMSEG 595	AMSEG 596	AMSEG 597	AMSEG 598	AMSEG 599	AMSEG 600	AMSEG 601	AMSEG 602	AMSEG 603	AMSEG 604	AMSEG 605	AMSEG 606	AMSEG 607	AMSEG 608	AMSEG 609	AMSEG 610	AMSEG 611	AMSEG 612	AMSEG 613	AMSEG 614	AMSEG 615	AMSEG 616	AMSEG 617	AMSEG 618	AMSEG 619	AMSEG 620	AMSEG 621	AMSEG 622	AMSEG 623	AMSEG 624	AMSEG 625	AMSEG 626	AMSEG 627	AMSEG 628	AMSEG 629	AMSEG 630	AMSEG 631	AMSEG 632	AMSEG 633	AMSEG 634	AMSEG 635	AMSEG 636	AMSEG 637	AMSEG 638	AMSEG 639	AMSEG 640	AMSEG 641	AMSEG 642	AMSEG 643	AMSEG 644	AMSEG 645	AMSEG 646	AMSEG 647	AMSEG 648	AMSEG 649	AMSEG 650	AMSEG 651	AMSEG 652	AMSEG 653	AMSEG 654	AMSEG 655	AMSEG 656	AMSEG 657	AMSEG 658	AMSEG 659	AMSEG 660	AMSEG 661	AMSEG 662	AMSEG 663	AMSEG 664	AMSEG 665	AMSEG 666	AMSEG 667	AMSEG 668	AMSEG 669	AMSEG 670	AMSEG 671	AMSEG 672	AMSEG 673	AMSEG 674	AMSEG 675	AMSEG 676	AMSEG 677	AMSEG 678	AMSEG 679	AMSEG 680	AMSEG 681	AMSEG 682	AMSEG 683	AMSEG 684	AMSEG 685	AMSEG 686	AMSEG 687	AMSEG 688	AMSEG 689	AMSEG 690	AMSEG 691	AMSEG 692	AMSEG 693	AMSEG 694	AMSEG 695	AMSEG 696	AMSEG 697	AMSEG 698	AMSEG 699	AMSEG 700	AMSEG 701	AMSEG 702	AMSEG 703	AMSEG 704	AMSEG 705	AMSEG 706	AMSEG 707	AMSEG 708	AMSEG 709	AMSEG 710	AMSEG 711	AMSEG 712	AMSEG 713	AMSEG 714	AMSEG 715	AMSEG 716	AMSEG 717	AMSEG 718	AMSEG 719	AMSEG 720	AMSEG 721	AMSEG 722	AMSEG 723	AMSEG 724	AMSEG 725	AMSEG 726	AMSEG 727	AMSEG 728	AMSEG 729	AMSEG 730	AMSEG 731	AMSEG 732	AMSEG 733	AMSEG 734	AMSEG 735	AMSEG 736	AMSEG 737	AMSEG 738	AMSEG 739	AMSEG 740	AMSEG 741	AMSEG 742	AMSEG 743	AMSEG 744	AMSEG 745	AMSEG 746	AMSEG 747	AMSEG 748	AMSEG 749	AMSEG 750	AMSEG 751	AMSEG 752	AMSEG 753	AMSEG 754	AMSEG 755	AMSEG 756	AMSEG 757	AMSEG 758	AMSEG 759	AMSEG 760	AMSEG 761	AMSEG 762	AMSEG 763	AMSEG 764	AMSEG 765	AMSEG 766	AMSEG 767	AMSEG 768	AMSEG 769	AMSEG 770	AMSEG 771	AMSEG 772	AMSEG 773	AMSEG 774	AMSEG 775	AMSEG 776	AMSEG 777	AMSEG 778	AMSEG 779	AMSEG 780	AMSEG 781	AMSEG 782	AMSEG 783	AMSEG 784	AMSEG 785	AMSEG 786	AMSEG 787	AMSEG 788	AMSEG 789	AMSEG 790	AMSEG 791	AMSEG 792	AMSEG 793	AMSEG 794	AMSEG 795	AMSEG 796	AMSEG 797	AMSEG 798	AMSEG 799	AMSEG 800	AMSEG 801	AMSEG 802	AMSEG 803	AMSEG 804	AMSEG 805	AMSEG 806	AMSEG 807	AMSEG 808	AMSEG 809	AMSEG 810	AMSEG 811	AMSEG 812	AMSEG 813	AMSEG 814	AMSEG 815	AMSEG 816	AMSEG 817	AMSEG 818	AMSEG 819	AMSEG 820	AMSEG 821	AMSEG 822	AMSEG 823	AMSEG 824	AMSEG 825	AMSEG 826	AMSEG 827	AMSEG 828	AMSEG 829	AMSEG 830	AMSEG 831	AMSEG 832	AMSEG 833	AMSEG 834	AMSEG 835	AMSEG 836	AMSEG 837	AMSEG 838	AMSEG 839	AMSEG 840	AMSEG 841	AMSEG 842	AMSEG 843	AMSEG 844	AMSEG 845	AMSEG 846	AMSEG 847	AMSEG 848	AMSEG 849	AMSEG 850	AMSEG 851	AMSEG 852	AMSEG 853	AMSEG 854	AMSEG 855	AMSEG 856	AMSEG 857	AMSEG 858	AMSEG 859	AMSEG 860	AMSEG 861	AMSEG 862	AMSEG 863	AMSEG 864	AMSEG 865	AMSEG 866	AMSEG 867	AMSEG 868	AMSEG 869	AMSEG 870	AMSEG 871	AMSEG 872	AMSEG 873	AMSEG 874	AMSEG 875	AMSEG 876	AMSEG 877	AMSEG 878	AMSEG 879	AMSEG 880	AMSEG 881	AMSEG 882	AMSEG 883	AMSEG 884	AMSEG 885	AMSEG 886	AMSEG 887	AMSEG 888	AMSEG 889	AMSEG 890	AMSEG 891	AMSEG 892	AMSEG 893	AMSEG 894	AMSEG 895	AMSEG 896	AMSEG 897	AMSEG 898	AMSEG 899	AMSEG 900	AMSEG 901	AMSEG 902	AMSEG 903	AMSEG 904	AMSEG 905	AMSEG 906	AMSEG 907	AMSEG 908	AMSEG 909	AMSEG 910	AMSEG 911	AMSEG 912	AMSEG 913	AMSEG 914	AMSEG 915	AMSEG 916	AMSEG 917	AMSEG 918	AMSEG 919	AMSEG 920	AMSEG 921	AMSEG 922	AMSEG 923	AMSEG 924	AMSEG 925	AMSEG 926	AMSEG 927	AMSEG 928	AMSEG 929	AMSEG 930	AMSEG 931	AMSEG 932	AMSEG 933	AMSEG 934	AMSEG 935	AMSEG 936	AMSEG 937	AMSEG 938	AMSEG 939	AMSEG 940	AMSEG 941	AMSEG 942	AMSEG 943	AMSEG 944	AMSEG 945	AMSEG 946	AMSEG 947	AMSEG 948	AMSEG 949	AMSEG 950	AMSEG 951	AMSEG 952	AMSEG 953	AMSEG 954	AMSEG 955	AMSEG 956	AMSEG 957	AMSEG 958	AMSEG 959	AMSEG 960	AMSEG 961	AMSEG 962	AMSEG 963	AMSEG 964	AMSEG 965	AMSEG 966	AMSEG 967	AMSEG 968	AMSEG 969	AMSEG 970	AMSEG 971	AMSEG 972	AMSEG 973	AMSEG 974	AMSEG 975	AMSEG 976	AMSEG 977	AMSEG 978	AMSEG 979	AMSEG 980	AMSEG 981	AMSEG 982	AMSEG 983	AMSEG 984	AMSEG 985	AMSEG 986	AMSEG 987	AMSEG 988	AMSEG 989	AMSEG 990	AMSEG 991	AMSEG 992	AMSEG 993	AMSEG 994	AMSEG 995	AMSEG 996	AMSEG 997	AMSEG 998	AMSEG 999	AMSEG 1000
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Table 3 (cont'd)

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Table 3 (cont'd)

Tissue	Tumor-txn	Normal-txn	Tumor-txn	Tumor-txn	Normal	Endos	p33	ISO M	ALISO 2	W1	SEG M	ALISO 43	NEISO 66	CA ISO 84	MH ISO 110	RISO 73	MR ISO 78	AM
784-0			126					851	4871	1571	1078		1272	1529		17251	20406	
T-470			182					533	9526	227	874		972	8836	5204	82291	33570	
Ren-3			171					5003	8510	0	1074	352	548					
Ren-3			183					0	1853	0	254	13	637					
7817 untreated + DMSO			171					278	3104	0	21	0	1787	130				
NS poly A+			187					187	1800	22	82	0	0					
PCOS poly A+			196					297	3059	0	108	0	1498	1618	650			
ACHN			196					297	3059	0	108	0	1498	1618	650			
UACC-62			196					0	6503	0	358	0	578	2815	860			
UACC-62			196					1493	6503	0	212	0	473	2225	2825			
UACC-62			196					183	3273	755	0	11	361	1444	2542			
UACC-62			196					0	7612	0	104	0	0	1028	0			
UACC-62			196					150	0	0	84	189	850	1028	0			
UACC-62			196					0	18178	0	523	32	0	2461	1447	916		
UACC-62			196					219	1868	0	236	0	34	261	1447	916		
UACC-62			196					271	3187	1198	206	0	0	261	1447	916		
UACC-62			196					0	5582	0	31	693	0	1065	83			
UACC-62			196					2280	21213	0	115	0	453	2918	158			
UACC-62			196					705	2006	0	115	0	453	2918	158			
UACC-62			196					521	4040	0	31	0	1303	2923	41			
UACC-62			196					0	2352	0	210	0	87	1773	1338			
UACC-62			196					646	6364	793	433	481	3528	3187	38419			
UACC-62			196					0	13083	0	526	73	1738	6402	159714			
UACC-62			196					14211	886	231	431	2402	3649	15999	38367			
UACC-62			196					1500	13017	3722	2945	167	3423	5366	85596	46201		
UACC-62			196					49	14320	498	179	0	304	691	1091	2285		
UACC-62			196					0	18144	0	510	304	691	1091	2285			
UACC-62			196					0	7267	383	0	23	244	2897	10221	17287		
UACC-62			196					0	107855	589	1456	0	150	1028	2424	7704	20878	
UACC-62			196					273	314	1330	0	189	473	905	1481	7813		
UACC-62			196					372	3084	0	0	0	0	0	0	0		
UACC-62			196					2585	9438	1811	625	52	142	347	1109	6		

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Table 3 (cont'd)

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Table 3 (cont'd)

Thema	Thema-ym	Normal-ym	Thema - te	Thema - mte	Normal	Endes	p22	SEG 34	AIJSD 37	WISD 40	AIJSD 43	NEJSD 44	CAJSD 45	WISD 116	WISD 73	WISD 74	AI
DaPheng-0	0	50728	3124	2203	0	2725	1021	16529	1194								
DaPheng-1	0	25361	84	3297	0	2819	7671	14951	14951								
DaPheng-11	0	25319	0	4208	0	4747	714	12727	12734								
DaPheng-12	0	40638	0	6123	0	3724	1086	43005	13175								
DaPheng-1	0	18013	0	1306	0	2184	882	68683	11807								
DaPheng-2	0	11728	0	24437	0	4720	801	34067	14401								
DaPheng-2	0	9271	0	13708	0	2678	1022	30201	21449								
DaPheng-5	0	8905	1171	9515	0	1528	793	15232	18156								
DaPheng-6	0	4989	0	216	0	303	1363	9271	2650								
AS1-1-8	0	3723	0	5101	0	1748	580	20142	25156								
EXVX-8	0	39564	0	0	0	1018	548	9031	12544								
HCT-116-7	mutant	0	6118	537	1675	0	2260	398	1927	3655							
HCT-116-8	mutant	0	6148	537	1675	0	2260	398	1927	3655							
HT29-1	mutant	0	2845	507	2081	0	43611	803	24764	14180							
HT29-7	mutant	0	5165	3418	899	0	812	478	841	13863							
HT29-8	mutant	0	2474	0	1863	0	302	391	114323	18908							
HT29-9	mutant	0	1063	0	0	0	1494	451	29516	21737							
SF353-8	mutant	0	4333	0	2992	0	307	209	8185	13162							
SF-263-7	mutant	0	8602	0	866	0	7001	504	15207	9784							
SF-353-8	mutant	0	8954	0	152	0	1074	108	12408	17680							
OVCA4-4-8	mutant	0	8910	1896	708	0	856	911	14378	18506							
OVCA4-5-8	mutant	0	8205	0	1884	0	1318	420	14248	15443							
OVCA4-5-9	mutant	0	1790	0	507	0	2052	568	6210	17401							
BCF-7-8	mutant	0	8000	789	12121	0	601	100	3378	14258							
ADIR-RES-8	mutant	0	8291	0	1758	0	3077	730	17300	18646							
SW480-2	mutant	0	3519	11046	48	0	18	1330	20056	33771							
SW480-3	mutant	0	4047	348	1309	0	279	228	8274	16851							
SW480-5	mutant	0	4033	1248	2005	0	842	451	15891	15472							
SW480-6	mutant	0	4132	914	1078	0	479	96	7975	12652							
H1298-8	mutant	0	28411	559	846	0	1023	708	14883	18305							
C3A-7	mutant	0	3995	366	1312	0	1028	712	13173	11466							
C3A-8	mutant	0	8441	8274	1442	0	215	458	18827	16113							
U2OS-7	mutant	0	4381	0	131	0	924	331	1082	11145							
U2OS-8	mutant	0	5463	306	458	0	1880	1422	8025	30298							
Hs6-7	mutant	0	4223	182	1921	0	1524	231	21451	18584							
Hs6-8	mutant	0	4253	17844	462	0	1488	614	24588	1923							
WI 38-2	mutant	0	4538	0	1109	0	306	614	10389	15141							
458 multiple RNA	mutant	0	8863	0	0	0	473	583	3369	17704							
CR1 1512 3/17/85	mutant	0	10478	0	4697	372	11543	2280	7101	12151							
Bea-4	mutant	0	1471	79	286	0	2368	889	1629	32153							
HT298	mutant	0	1359	7179	0	0	1482	969	32047	0							
HT298	mutant	0	415	16978	356												





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Table 3 (cont'd)

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Table 3 (cont'd)

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Tissue	Tumor type	Normal	Tumor	Tumor cells	Normal	Endoth	p53	SE0	SE1	SE2	SE3	SE4	SE5	SE6	SE7	SE8	SE9	SE10	SE11	SE12	SE13	SE14	SE15	SE16	SE17	SE18	SE19	SE20	SE21	SE22	SE23	SE24	SE25	SE26	SE27	SE28	SE29	SE30	SE31	SE32	SE33	SE34	SE35	SE36	SE37	SE38	SE39	SE40	SE41	SE42	SE43	SE44	SE45	SE46	SE47	SE48	SE49	SE50	SE51	SE52	SE53	SE54	SE55	SE56	SE57	SE58	SE59	SE60	SE61	SE62	SE63	SE64	SE65	SE66	SE67	SE68	SE69	SE70	SE71	SE72	SE73	SE74	SE75	SE76	SE77	SE78	SE79	SE80	SE81	SE82	SE83	SE84	SE85	SE86	SE87	SE88	SE89	SE90	SE91	SE92	SE93	SE94	SE95	SE96	SE97	SE98	SE99	SE100	SE101	SE102	SE103	SE104	SE105	SE106	SE107	SE108	SE109	SE110	SE111	SE112	SE113	SE114	SE115	SE116	SE117	SE118	SE119	SE120	SE121	SE122	SE123	SE124	SE125	SE126	SE127	SE128	SE129	SE130	SE131	SE132	SE133	SE134	SE135	SE136	SE137	SE138	SE139	SE140	SE141	SE142	SE143	SE144	SE145	SE146	SE147	SE148	SE149	SE150	SE151	SE152	SE153	SE154	SE155	SE156	SE157	SE158	SE159	SE160	SE161	SE162	SE163	SE164	SE165	SE166	SE167	SE168	SE169	SE170	SE171	SE172	SE173	SE174	SE175	SE176	SE177	SE178	SE179	SE180	SE181	SE182	SE183	SE184	SE185	SE186	SE187	SE188	SE189	SE190	SE191	SE192	SE193	SE194	SE195	SE196	SE197	SE198	SE199	SE200	SE201	SE202	SE203	SE204	SE205	SE206	SE207	SE208	SE209	SE210	SE211	SE212	SE213	SE214	SE215	SE216	SE217	SE218	SE219	SE220	SE221	SE222	SE223	SE224	SE225	SE226	SE227	SE228	SE229	SE230	SE231	SE232	SE233	SE234	SE235	SE236	SE237	SE238	SE239	SE240	SE241	SE242	SE243	SE244	SE245	SE246	SE247	SE248	SE249	SE250	SE251	SE252	SE253	SE254	SE255	SE256	SE257	SE258	SE259	SE260	SE261	SE262	SE263	SE264	SE265	SE266	SE267	SE268	SE269	SE270	SE271	SE272	SE273	SE274	SE275	SE276	SE277	SE278	SE279	SE280	SE281	SE282	SE283	SE284	SE285	SE286	SE287	SE288	SE289	SE290	SE291	SE292	SE293	SE294	SE295	SE296	SE297	SE298	SE299	SE300	SE301	SE302	SE303	SE304	SE305	SE306	SE307	SE308	SE309	SE310	SE311	SE312	SE313	SE314	SE315	SE316	SE317	SE318	SE319	SE320	SE321	SE322	SE323	SE324	SE325	SE326	SE327	SE328	SE329	SE330	SE331	SE332	SE333	SE334	SE335	SE336	SE337	SE338	SE339	SE340	SE341	SE342	SE343	SE344	SE345	SE346	SE347	SE348	SE349	SE350	SE351	SE352	SE353	SE354	SE355	SE356	SE357	SE358	SE359	SE360	SE361	SE362	SE363	SE364	SE365	SE366	SE367	SE368	SE369	SE370	SE371	SE372	SE373	SE374	SE375	SE376	SE377	SE378	SE379	SE380	SE381	SE382	SE383	SE384	SE385	SE386	SE387	SE388	SE389	SE390	SE391	SE392	SE393	SE394	SE395	SE396	SE397	SE398	SE399	SE400	SE401	SE402	SE403	SE404	SE405	SE406	SE407	SE408	SE409	SE410	SE411	SE412	SE413	SE414	SE415	SE416	SE417	SE418	SE419	SE420	SE421	SE422	SE423	SE424	SE425	SE426	SE427	SE428	SE429	SE430	SE431	SE432	SE433	SE434	SE435	SE436	SE437	SE438	SE439	SE440	SE441	SE442	SE443	SE444	SE445	SE446	SE447	SE448	SE449	SE450	SE451	SE452	SE453	SE454	SE455	SE456	SE457	SE458	SE459	SE460	SE461	SE462	SE463	SE464	SE465	SE466	SE467	SE468	SE469	SE470	SE471	SE472	SE473	SE474	SE475	SE476	SE477	SE478	SE479	SE480	SE481	SE482	SE483	SE484	SE485	SE486	SE487	SE488	SE489	SE490	SE491	SE492	SE493	SE494	SE495	SE496	SE497	SE498	SE499	SE500	SE501	SE502	SE503	SE504	SE505	SE506	SE507	SE508	SE509	SE510	SE511	SE512	SE513	SE514	SE515	SE516	SE517	SE518	SE519	SE520	SE521	SE522	SE523	SE524	SE525	SE526	SE527	SE528	SE529	SE530	SE531	SE532	SE533	SE534	SE535	SE536	SE537	SE538	SE539	SE540	SE541	SE542	SE543	SE544	SE545	SE546	SE547	SE548	SE549	SE550	SE551	SE552	SE553	SE554	SE555	SE556	SE557	SE558	SE559	SE560	SE561	SE562	SE563	SE564	SE565	SE566	SE567	SE568	SE569	SE570	SE571	SE572	SE573	SE574	SE575	SE576	SE577	SE578	SE579	SE580	SE581	SE582	SE583	SE584	SE585	SE586	SE587	SE588	SE589	SE590	SE591	SE592	SE593	SE594	SE595	SE596	SE597	SE598	SE599	SE600	SE601	SE602	SE603	SE604	SE605	SE606	SE607	SE608	SE609	SE610	SE611	SE612	SE613	SE614	SE615	SE616	SE617	SE618	SE619	SE620	SE621	SE622	SE623	SE624	SE625	SE626	SE627	SE628	SE629	SE630	SE631	SE632	SE633	SE634	SE635	SE636	SE637	SE638	SE639	SE640	SE641	SE642	SE643	SE644	SE645	SE646	SE647	SE648	SE649	SE650	SE651	SE652	SE653	SE654	SE655	SE656	SE657	SE658	SE659	SE660	SE661	SE662	SE663	SE664	SE665	SE666	SE667	SE668	SE669	SE670	SE671	SE672	SE673	SE674	SE675	SE676	SE677	SE678	SE679	SE680	SE681	SE682	SE683	SE684	SE685	SE686	SE687	SE688	SE689	SE690	SE691	SE692	SE693	SE694	SE695	SE696	SE697	SE698	SE699	SE700	SE701	SE702	SE703	SE704	SE705	SE706	SE707	SE708	SE709	SE710	SE711	SE712	SE713	SE714	SE715	SE716	SE717	SE718	SE719	SE720	SE721	SE722	SE723	SE724	SE725	SE726	SE727	SE728	SE729	SE730	SE731	SE732	SE733	SE734	SE735	SE736	SE737	SE738	SE739	SE740	SE741	SE742	SE743	SE744	SE745	SE746	SE747	SE748	SE749	SE750	SE751	SE752	SE753	SE754	SE755	SE756	SE757	SE758	SE759	SE760	SE761	SE762	SE763	SE764	SE765	SE766	SE767	SE768	SE769	SE770	SE771	SE772	SE773	SE774	SE775	SE776	SE777	SE778	SE779	SE780	SE781	SE782	SE783	SE784	SE785	SE786	SE787	SE788	SE789	SE790	SE791	SE792	SE793	SE794	SE795	SE796	SE797	SE798	SE799	SE800	SE801	SE802	SE803	SE804	SE805	SE806	SE807	SE808	SE809	SE810	SE811	SE812	SE813	SE814	SE815	SE816	SE817	SE818	SE819	SE820	SE821	SE822	SE823	SE824	SE825	SE826	SE827	SE828	SE829	SE830	SE831	SE832	SE833	SE834	SE835	SE836	SE837	SE838	SE839	SE840	SE841	SE842	SE843	SE844	SE845	SE846	SE847	SE848	SE849	SE850	SE851	SE852	SE853	SE854	SE855	SE856	SE857	SE858	SE859	SE860	SE861	SE862	SE863	SE864	SE865	SE866	SE867	SE868	SE869	SE870	SE871	SE872	SE873	SE874	SE875	SE876	SE877	SE878	SE879	SE880	SE881	SE882	SE883	SE884	SE885	SE886	SE887	SE888	SE889	SE890	SE891	SE892	SE893	SE894	SE895	SE896	SE897	SE898	SE899	SE900	SE901	SE902	SE903	SE904	SE905	SE906	SE907	SE908	SE909	SE910	SE911	SE912	SE913	SE914	SE915	SE916	SE917	SE918	SE919	SE920	SE921	SE922	SE923	SE924	SE925	SE926	SE927	SE928	SE929	SE930	SE931	SE932	SE933	SE934	SE935	SE936	SE937	SE938	SE939	SE940	SE941	SE942	SE943	SE944	SE945	SE946	SE947	SE948	SE949	SE950	SE951	SE952	SE953	SE954	SE955	SE956	SE957	SE958	SE959	SE960	SE961	SE962	SE963	SE964	SE965	SE966	SE967	SE968	SE969	SE970	SE971	SE972	SE973	SE974	SE975	SE976	SE977	SE978	SE979	SE980	SE981	SE982	SE983	SE984	SE985	SE986	SE987	SE988	SE989	SE990	SE991	SE992	SE993	SE994	SE995	SE996	SE997	SE998	SE999	SE1000	SE1001	SE1002	SE1003	SE1004	SE1005	SE1006	SE1007	SE1008	SE1009	SE1010	SE1011	SE1012	SE1013	SE1014	SE1015	SE1016	SE1017	SE1018	SE1019	SE1020	SE1021	SE1022	SE1023	SE1024	SE1025	SE1026	SE1027	SE1028	SE1029	SE1030	SE1031	SE1032	SE1033	SE1034	SE1035	SE1036	SE1037	SE1038	SE1039	SE1040	SE1041	SE1042	SE1043	SE1044	SE1045	SE1046	SE1047	SE1048	SE1049	SE1050	SE1051	SE1052	SE1053	SE1054	SE1055	SE1056	SE1057	SE1058	SE1059	SE1060	SE1061	SE1062	SE1063	SE1064	SE1065	SE1066	SE1067	SE1068	SE1069	SE1070	SE1071	SE1072	SE1073	SE1074	SE1075	SE1076	SE1077	SE1078	SE1079	SE1080	SE1081	SE1082	SE1083	SE1084	SE1085	SE1086	SE1087	SE1088	SE1089	SE1090	SE1091	SE1092	SE1093	SE1094	SE1095	SE1096	SE1097	SE1098	SE1099	SE1100	SE1101	SE1102	SE1103	SE1104	SE1105	SE1106	SE1107	SE1108	SE1109	SE1110	SE1111	SE1112	SE1113	SE1114	SE1115	SE1116	SE1117	SE1118	SE1119	SE1120	SE1121	SE1122	SE1123	SE1124	SE1125	SE1126	SE1127	SE1128	SE1129	SE1130	SE1131	SE1132	SE1133	SE1134	SE1135	SE1136	SE1137	SE1138	SE1139	SE1140	SE1141	SE1142	SE1143	SE1144	SE1145	SE1146	SE1147	SE1148	SE1149	SE1150	SE1151	SE1152	SE1153	SE1154	SE1155	SE1156	SE1157	SE1158	SE1159	SE1160	SE1161	SE1162	SE1163	SE1164	SE1165	SE1166	SE1167	SE1168	SE1169	SE1170	SE1171	SE1172	SE1173	SE1174	SE1175	SE1176	SE1177	SE1178	SE1179	SE1180	SE1181	SE1182	SE1183	SE1184	SE1185	SE1186	SE1187	SE1188	SE1189	SE1190	SE1191	SE1192	SE1193	SE1194	SE1195	SE1196	SE1197	SE1198	SE1199	SE1200	SE1201	SE1202	SE1203	SE1204	SE1205	SE1206	SE1207	SE1208	SE1209	SE1210	SE1211	SE1212	SE1213	SE1214	SE1215	SE1216	SE1217	SE1218	SE1219	SE1220	SE1221	SE1222	SE1223	SE1224	SE1225	SE1226	SE1227	SE1228	SE1229	SE1230	SE1231	SE1232	SE1233	SE1234	SE1235	SE1236	SE1237	SE1238	SE1239	SE1240	SE1241	SE1242	SE1243	SE1244	SE1245	SE1246	SE1247	SE1248	SE1249	SE1250	SE1251	SE1252	SE1253	SE1254	SE1255	SE1256	SE1257	SE1258	SE1259	SE1260	SE1261	SE1262	SE1263	SE1264	SE1265	SE1266	SE1267	SE1268	SE1269	SE1270	SE1271	SE1272	SE1273	SE1274	SE1275	SE1276	SE1277	SE1278	SE1279	SE1280	SE1281	SE1282	SE1283	SE1284	SE1285	SE1286	SE1287	SE1288	SE1289	SE1290	SE1291	SE1292	SE1293	SE1294	SE1295	SE1296	SE1297	SE1298	SE1299	SE1300	SE1301	SE1302	SE1303	SE1304	SE1305	SE1306	SE1307	SE1308	SE1309	SE1310	SE1311	SE1312	SE1313	SE1314	SE1315	SE1316	SE1317	SE1318	SE1319	SE1320	SE1321</
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Table 186  
Table 3 (cont'd)[illegible]



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Table 3 (cont'd)

Tissue	Turner - sym	Turner - asym	Turner - 10	Turner - 20	Normal	Endo	p33	SEQ 118	3
Testis								84	84
adrenal gland - h								822	822
thyroid gland - h								290	290
thyroid gland - h								235	235
thyroid gland - h								486	486
thyroid gland - h								237	237
thyroid gland - h								2719	2719
thyroid gland - h								1903	1903
thyroid gland - h								717	717
thyroid gland - h								162	162
thyroid gland - h								537	537
thyroid gland - h								348	348
thyroid gland - h								410	410
thyroid gland - h								0	0
thyroid gland - h								184	184
thyroid gland - h								514	514
thyroid gland - h								292	292
thyroid gland - h								260	260
thyroid gland - h								81	81
thyroid gland - h								167	167
thyroid gland - h								496	496
thyroid gland - h								884	884
thyroid gland - h								69	69
thyroid gland - h								141	141
thyroid gland - h								322	322
thyroid gland - h								28	28
thyroid gland - h								30	30
thyroid gland - h								3128	3128
thyroid gland - h								91	91
thyroid gland - h								188	188
thyroid gland - h								100	100
thyroid gland - h								0	0
thyroid gland - h								178	178
thyroid gland - h								11	11
thyroid gland - h								1030	1030
thyroid gland - h								102	102
thyroid gland - h								145	145
thyroid gland - h								123	123
thyroid gland - h								537	537
thyroid gland - h								140	140
thyroid gland - h								0	0
thyroid gland - h								0	0
thyroid gland - h								305	305
thyroid gland - h								361	361
thyroid gland - h								356	356
thyroid gland - h								354	354
thyroid gland - h								344	344
thyroid gland - h								342	342
thyroid gland - h								334	334
thyroid gland - h								332	332
thyroid gland - h								330	330
thyroid gland - h								328	328
thyroid gland - h								326	326
thyroid gland - h								324	324
thyroid gland - h								322	322
thyroid gland - h								320	320
thyroid gland - h								318	318
thyroid gland - h								316	316
thyroid gland - h								314	314
thyroid gland - h								312	312
thyroid gland - h								310	310
thyroid gland - h								308	308
thyroid gland - h								306	306
thyroid gland - h								304	304
thyroid gland - h								302	302
thyroid gland - h								300	300
thyroid gland - h								298	298
thyroid gland - h								296	296
thyroid gland - h								294	294
thyroid gland - h								292	292
thyroid gland - h								290	290
thyroid gland - h								288	288
thyroid gland - h								286	286
thyroid gland - h								284	284
thyroid gland - h								282	282
thyroid gland - h								280	280
thyroid gland - h								278	278
thyroid gland - h								276	276
thyroid gland - h								274	274
thyroid gland - h								272	272
thyroid gland - h								270	270
thyroid gland - h								268	268
thyroid gland - h								266	266
thyroid gland - h								264	264
thyroid gland - h								262	262
thyroid gland - h								260	260
thyroid gland - h								258	258
thyroid gland - h								256	256
thyroid gland - h								254	254
thyroid gland - h								252	252
thyroid gland - h								250	250
thyroid gland - h								248	248
thyroid gland - h								246	246
thyroid gland - h								244	244
thyroid gland - h								242	242
thyroid gland - h								240	240
thyroid gland - h								238	238
thyroid gland - h								236	236
thyroid gland - h								234	234
thyroid gland - h								232	232
thyroid gland - h								230	230
thyroid gland - h								228	228
thyroid gland - h								226	226
thyroid gland - h								224	224
thyroid gland - h								222	222
thyroid gland - h								220	220
thyroid gland - h								218	218
thyroid gland - h								216	216
thyroid gland - h								214	214
thyroid gland - h								212	212
thyroid gland - h								210	210
thyroid gland - h								208	208
thyroid gland - h								206	206
thyroid gland - h								204	204
thyroid gland - h								202	202
thyroid gland - h								200	200
thyroid gland - h								198	198
thyroid gland - h								196	196
thyroid gland - h								194	194
thyroid gland - h								192	192
thyroid gland - h								190	190
thyroid gland - h								188	188
thyroid gland - h								186	186
thyroid gland - h								184	184
thyroid gland - h								182	182
thyroid gland - h								180	180
thyroid gland - h								178	178
thyroid gland - h								176	176
thyroid gland - h								174	174
thyroid gland - h								172	172
thyroid gland - h								170	170
thyroid gland - h								168	168
thyroid gland - h								166	166
thyroid gland - h								164	164
thyroid gland - h								162	162
thyroid gland - h								160	160
thyroid gland - h								158	158
thyroid gland - h								156	156
thyroid gland - h								154	154
thyroid gland - h								152	152
thyroid gland - h								150	150
thyroid gland - h								148	148
thyroid gland - h								146	146
thyroid gland - h								144	144
thyroid gland - h								142	142
thyroid gland - h								140	140
thyroid gland - h								138	138
thyroid gland - h								136	136
thyroid gland - h								134	134
thyroid gland - h								132	132
thyroid gland - h								130	130
thyroid gland - h								128	128
thyroid gland - h								126	126
thyroid gland - h								124	124
thyroid gland - h								122	122
thyroid gland - h								120	120
thyroid gland - h								118	118
thyroid gland - h								116	116
thyroid gland - h								114	114
thyroid gland - h								112	112
thyroid gland - h								110	110
thyroid gland - h								108	108
thyroid gland - h								106	106
thyroid gland - h								104	104
thyroid gland - h								102	102
thyroid gland - h								100	100
thyroid gland - h								98	98
thyroid gland - h								96	96
thyroid gland - h								94	94
thyroid gland - h								92	92
thyroid gland - h								90	90
thyroid gland - h								88	88
thyroid gland - h								86	86
thyroid gland - h								84	84
thyroid gland - h								82	82
thyroid gland - h								80	80
thyroid gland - h								78	78
thyroid gland - h								76	76
thyroid gland - h								74	74
thyroid gland - h								72	72
thyroid gland - h								70	70
thyroid gland - h								68	68
thyroid gland - h								66	66
thyroid gland - h								64	64
thyroid gland - h								62	62
thyroid gland - h								60	60
thyroid gland - h								58	58
thyroid gland - h								56	56
thyroid gland - h								54	54
thyroid gland - h								52	52
thyroid gland - h								50	50
thyroid gland - h								48	48
thyroid gland - h								46	46
thyroid gland - h								44	44
thyroid gland - h								42	42
thyroid gland - h								40	40
thyroid gland - h								38	38
thyroid gland - h								36	36
thyroid gland - h								34	34
thyroid gland - h								32	32
thyroid gland - h								30	30
thyroid gland - h								28	28
thyroid gland - h								26	26
thyroid gland - h								24	24
thyroid gland - h								22	22
thyroid gland - h								20	20
thyroid gland - h									

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Table 3<sup>188</sup>  
(cont'd)

Tissue	Tumor type	Normal type	Tumor - 1a	Tumor cells	Normal	Endos	p53	SEQ 118 3
DAL-1				185				4
T-470				185				4
Leu-3				185				0
CRL 144 T RNA 8/90				171				0
761T untreated + DNase				181				72
KB poly A+				183				0
HOS poly A+				194				189
ACHN				195				47
LMCC-82				198				0
MCFT-7A (DR-RES)				200				53
UTOS (Mundy) poly A+				202				0
WISH (Collagen) poly A+				204				58
458 melanoma mRNA				206				0
COL 137 RNA 3/2/80				208				34
W138 T2h 0.5% FBS, 3h 10% FBS				218				200
CRL 1441 + TPA (2h) 8/90				219				0
Ren-1				220				0
Ren-2				220				242
Ren-3				221				0
HOP-82				223				46
MDA-T-4				225				74
SKVA				242				0
458				243				0
NCCH221				244				0
RPMI 8226				245				0
A549A TCC				246				0
SR				247				60
OVCA9-3				248				241
HCT-15				249				0
OVCA9-4				250				85
UO-31				251				180
OVCA9-5				252				0
SHYX				253				0
OVCA9-6				254				249
LO2 BMV				255				0
IGROV1				256				0
SK-MEL-3				257				0
SK-OV-3				258				0
SK-MEL-3				259				153
SK-SB				260				0
SK-MEL-28				261				0
H-562				262				0
LMCC-257				263				0
SK-14				264				60
MCFT				265				23
MDA-MB-435				267				49
HT779				268				0
MDA-MN				270				180
179 poly A+				271				0
MDA-MN poly A+				272				0
HT1338 2h TPA RNA 9/22				280				0
HELA-EXP-03/1880				300				26
HT1338 SK RNA				313				147
HT1347				322				83
458 melanoma RNA				323				0
NCCH225				324				0
HOP-80				326				152
MDA-MB-231				327				0
U251				328				0
PT cells poly A+				329				81
PC-3				340				0
HCC-2998				341				0
SW-620				343				0
HT152				345				0
COL O 205				346				0
HT178				347				148
MDA-12				348				0
HT151				349				0
A496				350				0
HT1203				351				36
RX2 283				352				0
TK-10				353				480
MDA-MB-3V				355				6
Hu 578T				356				263
HT1213				357				241
HT298			50	358				6
HT139			54					312
HT150			54					9
HT183			56					0
HT170			58					0
HT172			60					153
HT138			62					61
HT176			62					137
HT154			64					0
HT180			65					22
HT186			65					19
HT180			67					40
HT143			68					140
HT180			69					0
HT145			70					0
HT227			71					59
HT202			72					120
HT214			72					151
HT317			74					0
MDA-MB-435 RNA 8/25 1/80			76					0
HT323			77					0
HT327			78					0
HT325			80					21
HT146			82					137
HT348			83					9
HT311			87					98
HT306			170					29
HT140			185					18
HT251			187					0
HT372			189					0
TCOP			191					205
HT180			207					75
HT207			216					40
HT306			217					48
HT370			224					82
HT371			226					254
HT377			228					0
HT382			230					114
MDA-MB-435 RNA			236					125
HT334			291					113
HT338			299					468
HT392			301					231
HT394			313					0
HT312			317					80
HT182			318					0
HT209			325					0
HT157			354					0
T-470		183	360					46
MDA-MN		181						12
MDA-MB-435		155						63
MDA-MB-231		187						0

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Table 3 (cont'd)

Tissue	Tumor type	Normal stage	Tumor - %	Tumor cells	Normal	Endoth	p21	SE0 118 3
Ha 3787	155							0
MCF-7a DR-PC5	151							0
MCF-7	149							22
M14	147							0
LMCC-257	145							33
LMCC-42	144							0
SK-MEL-28	142							91
UO-31	142							4
SK-MEL-3	142							263
SK-M17	140							258
SK-MEL-2	139							181
HCT-116	138							250
Normal-30	137							0
COL-0203	136							0
LOX BAV	135							0
SW-620	134							0
TX-10	133							82
HCT 116	132							78
786-0	131							278
MCC-2048	130							0
ADPH	129							330
PC-3	128							80
DU-145	127							278
QJ-145	126							0
CAR-1	125							137
JA	124							0
AI-18	123							126
HPA-126	122							0
SH-2C	121							118
HL-40	120							0
MDA-T-4	119							36
QVCAR-1	118							642
K-562	117							898
QVCAR-4	116							181
CCRF-CEM	115							87
QVCAR-3	114							0
SF-438	113							183
PCP-42	112							110
SF-295	111							133
ASHBATCC	110							0
SF-294	109							204
NCI-H332	108							0
U251	107							30
NCI-H460	106							430
SNB-75	105							78
NCI-H322M	104							62
SNB-19	103							0
NCI-H24	102							777
SK-OV-3	101							0
KCLH2	100							54
IGROV1	99							0
BEV1	98							43
QVCAR-4	97							348
HOP-82	46							210
n. Rev. 10/1/92 #12	47							135
n. Rev. 10/1/92 #17	48							0
n. Rev. 10/1/92 #10	26							0
TCOP								379
AM18-1								458
AM18-3								347
AM18-4								73
AM18-5								86
AM18-7								200
BEVX-1								0
BEVX-4								483
BEVX-5								877
BEVX-6								0
BEVX-7								885
MCF-7-1								315
MCF-7-2								0
MCF-7-3								0
MCF-7-4								3049
MCF-7-5								150
MCF-7-6								79
ADR-RES-1								18
ADR-RES-2								90
ADR-RES-3								0
ADR-RES-4								283
ADR-RES-5								680
ADR-RES-6								880
ADR-RES-7								0
WI-38-1								0
WI-38-2								0
WI-38-3								0
WI-38-4								0
WI-38-5								0
WI-38-6								0
WI-38-7								0
IMB-1								0
IMB-2								0
IMB-3								0
IMB-4								0
IMB-5								0
IMB-6								0
IMB-7								0
HT29-1								0
HT29-2								0
HT29-3								183
HT29-4								0
HT29-5								0
HT29-6								0
AM18-2								820
EPV-2								80
HCT-116-1								0
HCT-116-2								0
HT29-7								0
SF-295-1								208
SF-295-2								631
SF-295-3								0
SF-295-4								0
QVCAR-1								523
QVCAR-2								208
QVCAR-3								86
QVCAR-4								221
QVCAR-5								173
ADR-RES-8								0
IMB-8								1083
SW-620-1								0
SW-620-2								0
HT29-8								271
CXA-1								537
CXA-2								0
LDOS-1								34
LDOS-2								298
IMB-9								0
IMB-10								0
WI-38-8								1450
IMB-11								532
IMB-12								0
IMB-13								0
IMB-14								0
IMB-15								0
IMB-16								0
IMB-17								0
IMB-18								0
IMB-19								0
IMB-20								0



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Table 4

Extra-Catalytic Domains (Amino acid positions)						
Gene Name	SP ID#	na ID#	aa	Family	Group	Length_AA
X69117_h beta_adrene	H	1	122	AGC	GRK	688
AA144574_m	M	2	123	AGC	GRK	378
AA210825_h	H	9	130	AGC	PKC	978
AA316804_h	H	11	132	AGC	PKC	890
AA887783_h	H	21	142	AGC	SGK	446
AA021445_h 3	H	32	152	CAMK	EMK	1311
R31237_1_h AAC3348	H	34	154	CAMK	EMK	729
406786.5_h	H	36	156	CAMK	EMK	1330
Z36720_h	H	41	161	CAMK	MLCK	874
SGK088_h	H	42	162	CAMK	Trio	2287
R19772_h	H	44	164	CAMK	Trio	1287
17000139801197_h IRAH	H	76	195	Other	IRAK	596
AA088547_h	H	78	197	Other	IRE	922
AA232253_h	H	82	201	Other	MLK	800
AA599286_h	H	89	208	Other	SLOB	649
AA836348_h	H	113	232	STE	NEK	836
PAK6_h	H	115	234	STE	STE20-02	719

Regulator of G protein signalling domain 54-175; PH domain 559-652

PH domain 249-337

Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577

Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532

PX domain 13-120

Vitamin K-dependent carboxylation/pantma-carboxylglutamic (GLA) domain 1072-1113

UBA domain 327-365

PAS domain 133-186, 247-280, 354-386

WD domain, G-beta repeat 674-711

Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779

RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528

Death domain 26-106

PQQ enzyme repeat 39-76

SAM domain (Sterile alpha motif) 337-408

PX domain 16-122

Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650

P21-Rho-binding domain 11-69

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## FIGURE 1A

SEQ ID NO: 122\_X69117\_H BARK2\_H

MADLEAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN  
 QKIGFLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC  
 SHPFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIQKFMESDKFTRFCQWKNV  
 ELNIHMTMNEFSVHRIIGRGGEVYGCRAKDTGKMYAMKCLDKKRIKMKOGETLALNER  
 IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE  
 IILGLEHVHNRFFVYRDLKPANILLDEHGHARISDLGLACDFSCKKPHASVGTHGYMAPE  
 VLQKGTAYDSSADWFSLGCMLFKLLRGHSPFRQHKTCDKHEIDRMTLTVNVELPDTFSPE  
 LKSLLEGLLQORDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVVYLQKYPPLIPPRGEVNAA  
 DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVTETVYEAVNADTDKIEARK  
 RAKNKQLGHEEDYALGKDCIMHGMYMLKGNPFLTQWQRRYFYLFNRLWRGEGESRQNL  
 LTMEQILSVEETQIKDKCILFRIKGGKQFVLQCESDPEFVQWKELNETFKEAQRLRLR  
 APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123\_AA144574\_M BARK2\_M

CFVVYRDLKPANILLDEYGHVRIIDLGLACDFSCKKPHASVGTHGYMAPEVLQKGTCTYDS  
 SADWFSLGCMLFKLLRGHSPFRQHKTCDKHEIDRMTLTVNQLPDAFSPELRSLLEGLLQ  
 RDVSQRLGCGGGGARELKEHIFFGIDWQHVVYLRYKYPPLIPPRGEVNAAADAFDIGSFDE  
 EDTGKIKLLDCDQDLYKNFPLVISERWQQEVETIYDAVNADTDKIEARKKAKNKQLGQE  
 EDYAMGKDCIMHGMYMLKGNPFLTQWQRRYFYLFNRLWRGEGESRQSLTMEQIMSVE  
 ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLRLRAPKFLNKPR  
 AILEFSKPLCHRNSNGL

SEQ ID NO: 124\_AA826850\_H

MGSSMSAATARRPVFDDKEDVNFDFHFIQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQ  
 QCIERDEVNRNVFRELEILQEIHEVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQ  
 FSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNIATIIKDGERA  
 TALAGTKPYMAPEIFXSFGVGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSSNAVESLV  
 QLFSTVSVQYVPTWSKEMVALLRKLTLNPEHRLSSLQDVQAAPALAGVLWDHLSEKRV  
 PGFVFNKGRHLCDPTFELEEMILESRLPHKKKKRLAKNRSRDNSSQSENDYLQDCLD  
 AIQQDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125\_AA960957\_H

MGGNHSKPPVFDENEEVNFDFHFIQILRAIGKGSFGKVCIVQKRDTKMYAMKYMKNQKCI  
 ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFT  
 GTVKLYICELALALEYLQRYHIHRDIKPDNILLDEHGHVHITDFNIATVVKGAERASSM  
 AGTKPYMAPEVFQVYMDRGPYSGYPVDWWSLGITAYELLRGWRPYEIHSTPIDEILNMF  
 KVERVHYSSTWCKGMVALLRKLTKDPESRVSSLHDIQSVPYLADMNWDVFKKALMPGF  
 VPKGRNLCDPTFELEEMILESRLPHKKKKRLAKNRSRDTGKDCPLNGHLQHCLETVRE  
 EFIIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNLLTHTCTRGCS

SEQ ID NO: 126\_TBK1\_H

MQSTSNHLWLLSDILGQATANVFRGRHKTGDLFAIKVFNNISFLRPVDVQMRFEFEVLK  
 KLNHNKIVKLFALIEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRDVV  
 GGMNHLRENGIVHRDIKPGNIMRVIAGEDQSVYKLTDFGAARELEDDEQFVSLEYGTEEYL  
 HPDMYERAVLRKDHQKYGATVDLWSIGVTIFYHAATGSLPFRPFEGPRRNKEVMYKIIIG  
 KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA  
 ETSAILHRMVIHVSFSLQOMTAHKIYIHSYNTATIFHELVIYKQTKIISSNQELIYEGRLV  
 LEPGRLAQHFPKTTENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITG  
 VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

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## FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSLADAWAHQE  
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYHATKAMTH  
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNELQETLPQ  
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHI LERFGSLTMD  
GGLRNVDCL

SEQ ID NO: 127\_AA305176\_H  
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGGKLYA  
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLOSANNVYLVMEYLIGGDVKS  
LLHIYGYFDEEMAVKYISEVALALDYLRHGI IHRDLKPDNMLISNEGHIKLTDFGLSKV  
TLNRDINMMDILTTPSMAPRODYSRTPGQVLSLISLGFNTPIAEKNQDPANILSACLS  
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS  
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128\_AA116841\_M  
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFV  
PQPDETDTSYFEARNNAQHLTVSGFSL

SEQ ID NO: 129\_AA256100\_H  
MAMTAGTTTTFPMNSNHTRERVTVAKLTLENFYNSNLIQHEERETRQKKLEVAMEEEGLAD  
EEKKLRRSQHARKETEFRLRLKRTLGLDDFESLKVIGRGAFGEVRLVQKDTGHIYAMKI  
LRKSDMLEKEQVAHIRAERDILVEADGAWVVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM  
KKDTLTEEETQFYISETVLAIDAIHQLGFIHRDIKPDNLLLDAGHVKLSDFGLCTGLKK  
AHRTEFYRNLTHNPPSDFSFQNMNSKRKAETWKKNRRLAYSTVGTPTYIAPEVFMQTGY  
NKLCDWWSLGVIMYEMLIGYPPFCSETPQETRYKVMNWKETLVFPPEVPISEKADLILR  
FCIDSENRIKNSGVVEIKGHPFFEGVDWEHIRERPAIPIEIKSIDTNSNDDFPESDIL  
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQGRSIPTYMKAGKL

SEQ ID NO: 130\_AA210825\_H  
DSLLPTPALGTPLPIWPVGSRLTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG  
SPLSHHLLTRSRGSRTOGPPGPPGGSRVGSRRVPGLPWPPPHYAGLPGPSGPGSP  
PPGGLQLQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQLACSIVDQKF  
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLSASATFEDFQIRPHAL  
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCGLNHYHKRCAFSIPNNCSGARKRRLSSTSL  
ASGHSVRLGTSESPLCTAEELSRSTELLPRRPSSSSSSASSYTGRPIELDKMLLSKV  
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDFNCHKRCATRVPNDCLEALIN  
GDVPMEEATDFSEADKSALMDESEDGVI PGSHSENALHASEEEEGEGGKAQSSLGYP  
MRVVQSVRHTTRKSSTTLREGWVHYNSKDTLRKRHYWRLDCKCITLFQNNNTNRYKEI  
PLSEILTVEAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX  
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSG  
QFGVVYGGKHKRTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLRHPGIVNLECMFETP  
EKVFVMEKLGDMLEMILSSEKGRLPRLTKFLITQILVALRHLHFKNIVHCDLKPENV  
LLASADFPQVKLCDFGFARIIGESFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVGVI  
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASWHSISAGAIIDLINLLQVKMRKRYSDK  
SLSHPWLOEQYTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA  
CPPQDHDMMQGLAERISVL

SEQ ID NO: 131\_AA127299\_H  
IQFIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKKTLTPTWNETFFVHFPEKTTLEL  
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

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## FIGURE 1C

SEQ ID NO: 132\_AA316804\_H

MSANNPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV  
SFLLOIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPÉCGFFGMYDKILLFRHDMNSEN  
ILQLITSADEIHEGDLVEVVLALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR  
QGLKCEGCGLNHYHKRCFAFKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLQPEYVALPSEES  
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM  
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSRSSRGLDDT  
EESPPEDEKMFLLDPSDLDERDEEAVKTI SPSTSNIPLMRVVQSIKHTKRKSSTMVKE  
GWMVHYTSRDNLKRHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQG  
SNPHCFEIIITDMVYFVGENNGDSSHPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV  
CTSPGQKDKHKLSTSI SVSNCOIQENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR  
DVAIKVIDKMRFPPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFFVMEKLHGDMLE  
EMILSSEKSRLEPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEPPQVKLCD  
FGFARIIGEKSFRRSVGTPAYLAPEVLRSGYNSRLDMWSVGVIYVSLSGTFPFNEDE  
DINDQIQNAAFMYPPNPWREISGEAIDLINLLQVKMRKRYSDKSLSHPLWLDYQOTWLD  
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133\_PKNBETA\_H

MEEGAPROPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRHGLGHVQQLRSS  
NRRLEQLHGELELHARILLPGPGPAEPVASGPRPWAEQLRARHLEALRRQLHVELKV  
KQGAENMTHTCASGTPKERKLLAAQQLRDSQLKVALLMKISSLEASGSPEPGPELLA  
EELQHRLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQQLQESSQKLDLLRLALEQLL  
EQLPPAHPLRSRVTRELRAAVPGYPQPSGTPVKPTALTGTQVRLGCEQLLTAVPGRSP  
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI  
PLERARELEIGVHWRDWRQLCGVAFLRLDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI  
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSPSTISPPKGCPR  
PTTLREADSPATPSNFLPKKTPLEEMTPPPKPPRLYLPQEPTEETPRTRKPHMEPRTR  
RGPSPPASPTRKPPRLQDFRCLAVLGRGHFGKVLVQFKGTGKYAIKALKKQEVLSRDE  
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSEHARFVTEFVPGGLMMQIHEDVFPEPQ  
ARFYVACVVLGLQFLHEKKIYRDLKLDNLLDAQGLFKIADFGCKEGIGFGDRTSTFC  
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPG  
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLC  
GPADLRYFEGETGLPPALTPPAPHSLLTARQQAARDFDFVSEFLEP

SEQ ID NO: 134\_AI021023\_M\_PKNBETA\_M

LKWDNLLLLDAQGLFKIADFGCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG  
LGVLLYEMLVGECPPFGDTEEEVFDCIVNMDAPYPGFLSVQGLEFIQKLLQKCPEKRLGA  
GEQDAEEIKVQPPFRTTNWQALLARTIQPPFVPTLCGPADLRYFEGETGLPPALTPPAP  
HSLLTARQQAARDFDFVSEFLEP

SEQ ID NO: 135\_H19102\_H

GGNIRGPWARGWKS LWTGLGTIRSDLEELWELRGHHYLHQESLKPAPVLVEKPLPEWPVP  
QFINLFLPEFPIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR  
DTRVQCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYSTDLYSLWSAVGCFPEASI  
RLFAAELVLVLCYLHDLGIMHRDVKMENILLDERGHLKLTDFGLSRHVPQGAQAYTICGT  
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERDHSVAMLASVTHSDSEIPAS  
LNQGLSLLLHELLCQNPLHRLRYLHFFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS  
SAETMPFDDFDCDLESFLLYPIPA

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## FIGURE 1D

SEQ ID NO: 136\_AA476563\_H  
MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTLPDGDASRSFNTSESKVEFKAQ  
DTISRGSDSDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN  
IGI IENKLLLEAPDVLCLRLSTEQCQ<sup>~</sup>AHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF  
VAAVDHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTESLFRICSPLSGANEYIASTDT  
LKTEEVLLFTDQDDLAKEEPTSLFQORDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS  
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILNDRGHIQLTYFSRWSEVEDS  
CDSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP  
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR

SEQ ID NO: 137\_AA626690\_H  
MLPFAPQDEPDREMEVFSGGGASSGEVNGLMVDEPMEEGEADSCHDEGVVKEIPITHH  
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT  
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA  
ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM  
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLPFQGDNRNETMNMILKAKLGMPOFLSAEA  
QSLLRMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF  
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEYKITPITSANVLPVQINGNAA  
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKI IDKSKRDPSEEIEILMRYGQHPNI  
ITLKDVFDDGRYVYLVTDLMKGGELLDRILKQKCFSEREASDILYVISTVDYLHCQGVV  
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGILLTPCYTANFVAPEVLMQQGYD  
AACDIWSLGLVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNI SDGAKDLL  
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ  
PVLEPVAASSLAQRRSMKKRTSTGL

SEQ ID NO: 138\_AA215680\_H  
MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPDMTKRDYLVDAATQIRLA  
LERDVSEDIYEA AFNHYQNGVDVLLRGIHVDPNKERREAVKLKITKYLRRAEI FNCHLQR  
PLSSGASPSAGFSSLRLRP IRTLSSAVEQLRGCRVVGVI EKVLVQDPATGGTFVVKSLP  
RCHMVSRRERTI IPHGVPYMTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL  
SSGSTQERMKAQLNPHLNLTPARLP SGHAPGQDRIALEPRTSPNLL LAGEAPSTRPQR  
EAEGEPTARTSTSGSSDL PKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG  
RGMDQSCLSADGAGRGCRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL  
DQAGHIRLTYFGQWSEVEPQCCGEAVDNL YSAPEVGGI SELTEACDWW SFGSLLYELLTG  
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRR LGMGEGGVSKLKSHPFFS  
TIQWSKLVG

SEQ ID NO: 139\_SGK\_H  
MTVKTEAAKGTLTYSRMGMVAILIAFMKQRRMGLNDFIQKIANN SYACKHPEVQSILKI  
SQPQEPELMNANPSPPPSPSQQINLG PSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA  
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHFSFQTADKLYFVLDYIN  
GGELFYHLQQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYR  
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW  
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG  
FSYAPPTDSFL

SEQ ID NO: 140\_AA107515\_M  
MTVKAEAAARSTLTYSRMGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM  
SHPQEPELMNANPSPPPSPSQQINLG PSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA

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## FIGURE 1E

EVFYAVKVLQKKAAILKKKEEKHIMSERVLLKNVKNHPFLVGLHFSFQTADKLYFVLDYIN  
GGELFYHLQORERCFLPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD  
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN  
TAEMYDNI LNKPQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD  
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF  
SYAPPVDSFL

SEQ ID NO: 141\_AA109508\_M  
HLQORERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE  
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY  
ENILHQPLQIPGGRTVAACDLLQSLHKKDQORQLGSKADFLEIKNHVFFSPINWDDLYHK  
RLTPPFNPVNTGPADLKHFDPFTEQEA VSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD  
ILDC

SEQ ID NO: 142\_AA887783\_H  
MQRDHTMDYKESCPVXIPSSDEHREKKKRFTVYKVLVSVGRSEWVFRRYAEFDKLYNT  
LKKQFPAXALKIPAKRIFGDNFDPDFIKORRAGLNEFIQNLVRYPELYNHPDVRAFLQMD  
SPKHQSDPSEDEDERSSQKLHSTSONINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLAK  
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKNHPFLVGLHYSFOTTEKLYFVL  
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTPEYLAPEVIRKQPYDNTVDWWCLGAV  
LYEMLYGLPPFYCRDVAEMYDNI LHKPLSLRPGVSLTAWSI EELLEKDRQNRLGAKEDF  
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTEETVPYSVCVSSDYSI  
VNASVLEADDAFVGFSYAPPSDLFL

SEQ ID NO: 143\_R47805\_H  
MAHOTGIHATEELKEFFAKARAGSVRLIKVVIDEQVLVGASQEPVGRWDQDYDRAVLPL  
LDAQQPCYLLYRLDSQNAQGFEWLFLAWS PDNSPVRLKMLYAA TRATVKKEFGGHIKDE  
LFGTVKDDLSFAGYQKHLSSCAAPAPLTSARELQQIRINEVKTEISVESKHQTLQGLAF  
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL  
YKHTHEGDPLESVVFYISMPGYKCSI KERMLYSSCKSRLDSVEQDFHLEIAKKIEIGDG  
AELTAFLYDEVHPKQHAFKQAFAPKPGPGGKRGHKRLIRGPGENGDD

SEQ ID NO: 144\_H60215\_H  
MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR  
KDGTDDFYQLKILTLEERGDOGIESQEERQGM L LHT EYSLLSLLHTQDGVVHHHGLFQD  
RTCEIVEDTESSRMVKKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV  
VIFYDVVRVVEALHQKNIVHRDLKLGNMVNLNRTHRITITNFC LGKHLVSEG DLLKDQRG  
SPAYISPDVLSGRPYRGKPSDMWALGVVLTMLYQGFPFYDSIPQELFRKIKAAEYTIPE  
DGRVSENTVCLIRKLLVLDPOQR LAAADVLEALSAI IASWQSLSSLSGPLQVVPDIDDQM  
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRLGH  
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145\_SGK324\_H  
MASTRSIELEHFEERDKRPRPGSRRGAPSSSGGSSSSSGPKGNGLIPSPAHSACSFYRTR  
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV  
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDTKNINPNWSVNIKGGSRALAAA  
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASG  
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS  
RSSAVKYSKSGKSPGSRRSQISAHGRSSSNVNGGPELDRCISPEGVNGNRCSESSTLLEK  
YKIGKVI GDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

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## FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH  
 RDIKPENLLVCEYPDGTSKSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD  
 IWAAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ  
 VNVEARCTAGQILSHPWVSDASQENNMQAEVTGKLKQHFNNALPKQNSTTTGVSIVMVS  
 GRRQVWPDCGAGLEVFEGLSRELPSHGWSCLP

SEQ ID NO: 146\_W30246\_M SGK324\_M  
 TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPEGVNGNRCSESFPLLEKYR  
 IGKVIDGDNFAVVKECVDRYTGKEFALKI IDKAKCCGKEHLIENEVSILRRVKHPNIIML  
 VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHLSLIVHRD  
 IKPENLLVCEYPDGTSKSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW  
 AAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147\_AA383293\_H  
 PAAKRVVYRNGDPFFPGSQLVVTQRRFPTMEAFCEVTSVQAPLAVRALYTPCHGHPV  
 TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFFSLKLSQAASQDWETVL  
 KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA  
 GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTKYQQSETSRDQSFPSGVIGVYGA  
 PHRRKETAGALEVADDEDQTTEEPLDQRAAQIVEQVTCLODFGDDDFIACGPEKFRYA  
 QDDFVLDHSRRRLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGRRMTLRDDQPAKLEK  
 EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA  
 MKIIDSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI  
 IESVKFPEPDAALMIMDLCKALVHMHDKSI VHRDLKPENLLVQRNEDKSTTLKLADFGLA  
 KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPXXGDQDE  
 LFNI IQLGHFELPPYWDNISDAKDLVSRLLVVDPPKRYTAHQVLQHPWIETAGKTNTV  
 KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148\_AA197883\_M  
 MPTAPVLRPPPPATPAPPAPSRPAPPIPGHRGPCDHSLKCLSSKISERKLPGPWLPAGR  
 GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVTVVKLGQPLRKATLLNRRS  
 VQTFEQLLSISEALGFPRWKNDVRKLF TLKGREVKSVSDFFREGDAFIAMGKEPLTLK  
 SIQLAMEELYPKNRALALAPHSRVPSRLRSRLPSKLLKGSHRCEAGSYSAEMESKAVS  
 RHQGTSTVLAPEDKARAQKWVRGKQSEPGGPPSPAATQEETHASGEKHLGVEIEKTS  
 GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD  
 GEEGWKGDShrgSPRDPPQEMRRPNSNSDKKEIRGSESQDSYPQAPKAQKDFVEGPPAV  
 EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPQLPRTRGEEKQAEHEKKPGGLGERAPE  
 KESKRKLEEKRPERSGRKPRPKGII SADVEKHYDIGGVI GDGNFATVKECRHRETKQAY  
 AMKMIDKSQLKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA  
 IVENVKFPEPEAAVMITDLCKAFVHMHDKNI VHRDVKPENLLVQRNEDKSTTLKLADFG  
 AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPERDQDE  
 LFNI IQVGQFEFLSPYWDNISDAKDLVRNLLVDPKKRYTAEQVLQHPWIEMVGHTNTG  
 NSQKEESPNLGHFQSQHKKVAEQMP

SEQ ID NO: 149\_DRAK2\_H  
 MSRRRFDCRSISGLLTTPQIPIKMENFNIFYILTSKELGRGKFAVVRQCISKSTGQEYA  
 AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS  
 LCLPELAEMVSENDVIRLIKQILEGVYYLHQNINIVHLDLKPONILLSSIIYPLGDIKIVDF  
 GMSRKIGHACELREIMGTPEYLAPEILNYDPITTTATDMWNIGI IAYMLLTHTSPFVGEDN  
 QETYLNI SQVNDYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWQQWDFEN

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## FIGURE 1G

LFHPEETSSSSQTQDHSVRSSSEDKTSKSSCNGTCGDREDKENI PEDSSMVSKRFRFDDSL  
PNPHELVSDDL C

SEQ ID NO: 150\_W44160\_M DRAK2\_M  
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA  
AKSLKKRRRGQDCRAEILHEIAVLELARSCHVINLHEVYENATEIILVLEYAAGGEIFN  
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNINIVHLDLKPQNILLSSIIYPLGDIKIVDF  
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN  
QETYNISQVNVVDYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS  
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENI PEDGSLVSKRFRFDDSL  
PSPHELVPDLFC

SEQ ID NO: 151\_H01248\_H, DRAK1\_H  
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS  
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRKGQDCRMEI IHEIAVLELAQDNPW  
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR  
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI  
SMATDMWSIGVLTIVMLTGISPFLGNDKQETFLNISQMNLSYSEEFVDLSESVDVFIRT  
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDDTKSE  
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAI SKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152\_AA021445\_H  
MPARIGYYEIDRTIGKGNFAVVKRATHLVTKAKVAIKI IDKTQLDEENLKKI FREVQIMK  
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF  
CHCRNI VHRDLKAENLLLDANLNKIADFGFSNFTPGQLLKTWCGSPPYAAPELFEGKE  
YDGPKVDIWSLGVVLYVLVCGALPFDGSTLQNLRLARVLSGKFRIPFFMSTECEHLIRHML  
VLDPNKRLSMEQICKHKWMLGDADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL  
DKEQTLQSLRSDAYDHYSIYSLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG  
TAMNISVPQVQLINPENQIVEPDGTLNLDSEGEEPSPEALVRYLSMRHTVGVADPRTE  
VMEDLQKLLPGFPGVNPQAPFLQVAPNVNFMHNL LPMQNLQPTGQLEYKEQSLQPPTLQ  
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ  
EAVQRYLANRSKRHTLAMTNPTAEI PPDLQRLGQQPFRSRVWPHLVPDQHRSTYKDSN  
TLHLPTERFSPVRRFSDGAASIQAFAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT  
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQSPPLQAACENQALLTHQLQRLRIQPS  
SPPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSIIFQQQPENCSSPPN  
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL  
MATLSYGHRPLSKQLSADSAEAHSLNVNRFSPANYDQAHLPPLFSDQSRGSPSSYSPST  
GVGFSPTQALKVPLDQFPTFPFSAHQPPHYTTSAQQALLSPTPPDYTRHQQVPHILQ  
GLLSRPHSLTGHSDIRLPTEFAQLIKRQQQQRQQQQQQQQQEQELFRHMNQGDAGSL  
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHGYAHQPALM  
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG  
IHPYGHQPTAAFSKNKVPSPREPIGNCMDRSSPGQAVELPDHNLGYPARPSVHEHHRPR  
ALQRHHTIQNSDDAYVQLDNLPGMSLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE  
CGASLGGHEHPDLSDGSLNSSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153\_2R22-5-11\_H  
MTAVYMNGGGLVNPHYARWDRRDSVESGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK  
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGHSITKEKVAIKILDKTKLDQKTQRLLSR  
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI  
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

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## FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR  
LIRGVLOQIPTERYGIDCIMNDEWMQGVPTPLEPFQLDPKHLSETSTLKEEENEVKST  
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPMMLPDPKERDLKKS  
RVYRGIRHTSKFCSIL

SEQ ID NO: 154\_R31237\_1\_H, AAC33487  
MSTRTPLTVNERTDENTHTSHGDRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLLK  
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLQKLFREVRIMKILNHPNIVKLFE  
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK  
AENLLLDADMNIAIDFGFSNEFTVGGKLDTCGSPPYAAPLFGQKKYDGPVVDVWSLG  
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFVLVLPNPIKRGTLQ  
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT  
YLLLGKRSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQRSVSSSQKQRRYS  
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPLGNASPNK  
ADIPERKKSSTVPSSNTASGGMTRRNTYVCSERTTADRHSVIQNGKENSTIPDQRTFVAS  
THSISAAATPDRI RFPRTASRSTFHGQPRERRATYNGPPASPSLSHEATPLSQTRSRG  
STNLFSKLTSLKTRSRNVSAEQKDENEAKPRSLRFTWSMKTTSMDPGDMMREIRKVL  
ANNCDYEQRRERFLLFCVHGDGHAENLVQWEMEVCKLPRLSLNGVRFKRISGTSIAFKNIA  
SKIANELKL

SEQ ID NO: 155\_W90839\_M  
KGPSWSSRSLGARCRNSIASCPEEQPHVGNRYRLLRTIGKGNFAKVKLARHILTGREVAIK  
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLIMEYASAGEVFDYLV  
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLDAAENIKIADFGFSNEFTL  
GSKLDTFCGSPPYAAPLFGQKKYDGPVVDIWSLGVILYTLVSGSLPFDGHNKELRERV  
LRGKYRVPFYMSTDCESILRRFLVLNPAKRTLEQIMKDKWINIGYEGEELKPDTELKEE  
RMPGRKASCASVSGSRGLPPSSPMVSSAHNPNAEIPERRKDSTSTPNNLPPSMMTRRN  
TYVCTERPGSERPSLLPNGKENS SGT SRVPPASPSHSLAPSGERSRLARGSTIRSTFH  
GGQVRDRRAGSGGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSLKTRRVTD  
PERIGGPEVTSCHLPWDKTETAPRLLRFPWSVKLTSSRPS

SEQ ID NO: 156\_406786.5\_H  
MEVGGLTVFEEDQRCLSQLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSRLCQS  
RTALSEDRWSSYCLSSLAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRGLSSGWSS  
PLLPAVPCNPNAIFTVDKTTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVVE  
ALSEEHMEADGHAAVFGTVVDIITRSGEKIPVSVMKMRMRQERRCCVVVLEPVERVST  
WVAFQSDGTITSCDSLFAHLHGYVSGEDVAGQHITDLIPSVQLPPSGQHIKPNLKIQRV  
GRARDGTTFFPLSLKLSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI  
NHSFALTFLGYGKTELLGKNITFLIPGFYSYMDLAYNSSQLPDLASCLDVGNESGGER  
TLDPWQGGQDPAEGGQDPRINVVLGGHVPRDEIRKLMESQDIFTGTQTELIAGGQLLSC  
LSPQAPAGVDNVPESLPPVHGEQALPKDQOITAGREEPVAIESPGQDLLGESRSEPDV  
KPFASCEDSEAPVPAEDGSDAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ  
LAGGSLLMHCPCYGESEWGLWWSQDLAPSPSGMAGLSFGTPTLDEPWLGVENDREELQTC  
LIKEQLSQLSLAGALDVPHAEVLPTECQAVTAPVSSCDLGGRLCGGCTGSSSACYALAT  
DLPGGLEAVEAQEVDVNSFSWNKELFFSDQTDQTSNCS CATSELRETPSSSLAVGSDPD  
VGSLOEQGSCVLDRELLLTGTCDVLDGQGRFRESVGHDPTEPLEVCLVSEHYAASD  
RESPGHVPSTLDAGPEDTCSAEPRNLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH  
RDGLRLSIQFEVRRVELQGPTPLFCCWLKDLLHSQRDSAARTRFLASLPGSTHSTAAE  
LTGPSLVEVLRARPWFEEPPKAVEGLEGAACEGEYSQKYSTMSPLGSGAFGVWTAVDKG  
KNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLTAIILSRVEHANI KVLDFENQGGFFQLV

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## FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDIHRDIKDEN  
 IVIAEDFTIKLIDFGSAAYLERGKLFYTCGTIEYCAPEVLMGNPYRGPELEMWSLGVTL  
 YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVDPWVTQ  
 PVLADYTWEVFRVKNKPESGVLASALEMGNRSLSDVAQAQELCGGPVGEAPNGQGCL  
 HPGDPRLLTS

SEQ ID NO: 157\_AA544838\_M 406786\_M  
 TRPHPCLDPLASFIFRQLVSAVGYLHSQGIHRDIKDENIVIAEDFTIKLIDFGSAAYL  
 ERGKLFYTCGTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV  
 IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIIRDWPVTQPVNLASYTWEVCRTNQPS  
 GLLSAASLEIGSRSPSEMAQREGLCGPPAPRETRGDQHCLHLKDPSLPVS

SEQ ID NO: 158\_AA785735\_H  
 MVMADGPRHLQRPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKIIDKSQLDVN  
 LEKIYREVQIMKMLDHPHIIKLYQVMTKSMYLVTEYAKNGEIDYLANHGRNLNESEAR  
 RKFQWILSAVDYCHGRKIVHRDLKAENLLDNNMNIKIADFGFGNFFKSGELLATWCGSP  
 PYAAPEVFEGQQYEGPQLDIWSMGVVLVLCGALPFDGPTLPILRQVRLEGRFRIPYFM  
 SEDCEHLIRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV  
 LRLMHSGLIDQOKXIESLQNKSYNHFAAIYFLLVERLKSRRSFPVEQRLDGRQRRPSTI  
 AEQTVAKAQTVGLPVTMHSNMRLLRSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT  
 PKVNGCLLDVPPVLRKGCQSLPSNMETSIDEGLETEGEAEEDPAHAFAEFQSTRSGQ  
 RRHTLSEVTNQLVVMGAGKIFSMNDSPLSDSVSEYDMGSVQRDNLNFDENPSLKDIML  
 ANQPSPRMTSPFISLRPTNPAMQALSSQKREVHNRSPVSFREGRRASDTSLTQGIVAFRQ  
 HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAPQLQDLASSCPQEEVSQQQESVST  
 LPASVHPQLSPRQSLQYLOHRLQKPSLLSKAONTQOLYCKEPPRSLEQQLOEHLRQKQK  
 RLFLQKQSQLQAYFNQMQUIAESSYPQPSQQLPLPRQETPPPSQQAAPPFSLTQPLSPVLEP  
 SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA  
 PLQFSYQTCELPSAASPAPDYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL  
 SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159\_AA207220\_H  
 MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRRHYEFLETGLG  
 KGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHIIAIEHVEFE  
 NSSKIVIVMEYASRGDLYDIISERQQLSREARHFFRQIVSAVHYCHQNRVVRDLKLEN  
 ILLDANGNIKIADFGLSNLYHQGKFLQTCGSPLYASPEIVNGKPYTGPEVDSWSLGVLL  
 YILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS  
 HWWVNWGYATRVGEQAPHEGGHPGSDSARASMAWLRSSRPLENGAKVCSFFKQHAP  
 GGGSTTPGLERQHSLLKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGKILKKKVSASA  
 EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSESSELDDAGDVV  
 SGDPKEQKPPQASGLLLHRKGILKLNKFSQTALELAAPTTFGSLDELAPPRPLARSRP  
 SGAVSEDSILSSESFQDLDPERLPEPPLRGCVSDNLTGLEEPPSEGGPSCLRRWRQDP  
 LGDSCFSLTDCQEVATYRQALRVCSKLT

SEQ ID NO: 160\_AA426580\_H, MAK\_V\_H  
 MPAAAGDGLLGEPAAPGGGGAEDAARPAACEGSFLPAWVSGVPRERLRDFQHHKRVGN  
 YLIGSRKLGECSFAKVREGLHVLTKGKVAIKVIDKKRAKDTYVTKNLRREGQIQQMIRH  
 PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA  
 GVVRDLKIEENLLDDENNIKLIDFGLSNCAGILGYSDPFSTQCGSPAYAAPELLARKKY  
 GPKIDVWSIGVNMAMLTGTLPFTVEPFLRALYQKMVDKEMNPLPTQLSTGAISFLRSL  
 LEPDPVKRPNIQQALANRWLNENYTGKVPNCVTYPNRI SLEDLSPSVVLHMTEKLGKNS

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FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKTRLYQIEKYRAPKESYEA  
SLDTWTRDLEFHAVQDKKPKKEQKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA  
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNVASSSMEFIPVPPRTPRIVKKPEPHQP  
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHYRILNSPVSLARRNSSERTLS  
PGLPSGMSPLHTPLHPTLVSFADHDKNSPPKEEGLCCPPVPVPSNGPMQPLGSPNCVKSR  
GRFPMMGIGQMLRKRHQSLSQPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161\_Z36720\_H  
MDTKLNLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI  
DTQAGWPEVLELVAMQDAAQHGARLEALFRMVAAVDRAIALVGATFQKSKVADFLMQG  
RVPWRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQDKGELSAEQGIWATLMTLV  
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG  
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAGRVNV  
VSPSLEVAPGAGQGASSRPDPEPLEEGTRLTGPGPGQCPGPPGLPAQARATHSGGETPP  
RAALLKGAVAPGFSRRDLVFPISIFCACLGISIHQEMDTPGEMLMTGRGSLGTLTTEAP  
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEEQRAGAEPG  
TRPSLARSDDNDHEVGALGLQQKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEGSV  
VLDDSPAPPAPFEHRVVSVKETSISAGYEVQCHEVLGGGRFGQVHRCTEKSTGLPLAAKI  
IKVKSADREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK  
YHTELDVVLFTTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP  
REKLKVNFGTPEFLAPEVVNYEFVSFTDMWSVGVI TYMLLSGLSPFLGETDAETMNFIV  
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNNLPKASRSKTRLK  
SQLLLQKYIAQRKWKKHFFYVVTAANRLRKFTSP

SEQ ID NO: 162\_SGK088\_H  
GEMALFECLVAGPTDVEVDWLCRGRLLOPALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC  
KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVTWTHFG  
CPMEESLENRLRQDGLHSLHIAHVGEDEGLYAVSAVNTHGQAHC SAQLYVEEPRTAAS  
GPSSKLEKMPSIPEEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW  
FHNGHRIQSSDDRMTQYRDVHRLVFPVAGPQHAGVYKSVIANKLGAACYAHLVYTDVV  
PGPPDGAPQVAVTGRMVTLTNPPRSLDMAIDPDSLTYTVQHQLGSDQWALTGLRE  
PGWAATGLRKGVQHI FRVLSTTVKSSSKSPSEPVLLEHGPTLEEAPAMLDKPDIVYV  
VEGQPASVTVTFNHVEAQVVRSCRGALLEARAGVYELS QPDDQYCLRICRVSRDMGA  
LTCTARNRHGTQTC SVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDMWYKD  
EVLLTESSHVSFVYEENEC SLVVLSTGAQDGGVYTCTAQN LAGEVSCKAELAVHSAQTAM  
EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFI PSQAKPKAS  
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLER IARKPTVCESEIRAYMR  
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCYGTF  
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFVGENDRITLMNIRNYNVAFEETTF  
LSLSREARGFLIKVLVQDRLRPTAETLEHPWFKTQAKGAEVSTDHLKFLSRRRWQRSQ  
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP  
EFGSGRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEA PSPEALPSPGQEPAA  
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG  
EYARQLQALRQRLLRGGPEDGKVSGLRGP LLES LGGRARDPRMARAASSEAPHHQPPE  
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPSSPARP  
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVRA SKPAPPQALQTLALP  
LTPYAQIIQSLQLSGHAQGPSQGPAAAPPSEPKPHA AVFARVASPPGAPKEKRVPSAGGPP  
VLAEKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG  
PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRTF  
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQSRGSSSEDSSGGAS

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## FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES  
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPVFHIIKLKDQVLLEGEAA  
 TLLCLPAACPAPHISWMKDKSLRSEPSVIIVSKDGRQLLSIPRAGKRHAGLYECSATN  
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQDTALVLWKPGDSRAPCTYTLERRVDGESVW  
 HPVSSGIPDCYINVTHLPVGVTVRFRVACANRAGQGPFNSSEKVFVRGTQDSSAVPSAA  
 HQEAPVTSRPARARPPDSPSTSLAPPLAPAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP  
 PQTPPRRHRGLQAARPAEPTLPSTHVTTPSEP KPFVLDTGTPIPASTPQGVKPVSSSTPVY  
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP  
 PQKPYTFLEEKARGFRGVVRACRENATGRTFVAKIVPYAAEGKPRVLQEYEVLRTLHHER  
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFRYSEDDVATYMVQLLOGLDYLHGHV  
 LHLDIKPDNLLLAPDNALKIVDFGSAQPPYNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA  
 TDIWAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFADFOLYPNTSQSATLFLRKVLSV  
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLLR  
 SYPGGP

SEQ ID NO: 163\_AA542015\_M SGK088\_M  
 ATDIWAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFADFOLYPNTSQSATLFLRKVLS  
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLL  
 RSYPGSP

SEQ ID NO: 164\_R19772\_H  
 MKGGDRAYTRGPSLGWLFKCCCCFPCTDAYSHSSSENGGKSESVANLQAQPSLNFIIHSS  
 PGKRSTNTLKKWLTSPVRRNLNSGKADGNIIKKQKKVRDGRKSF DLGSPKPGDETTPQGDS  
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA  
 IEKLVKNKLSLEGSSYRGLSKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVNLV  
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGDKIVFGNIHQIYDWHKDFFLAELEKCI  
 QEQDRLAQLFIKHERKLHIYVWYQCNKPRSEYIVAEYDAYFEEVKQEI NRRLTSDFLIK  
 PIQRITKYQLLLKDFLYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGRLOGFEGTTLT  
 AQGKLLQODTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN  
 YLVLEENVNDNDPCKFALMNRETSE RVVLQAANADIQQA WVDINQVLETQYRDFLNLQSP  
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPKISTNSGSP  
 GFEYHQPGDKFEASKNDLGCGNGTSSMAVIKDYYALKENEICVSQGEVVQVLAVNQNM  
 LVYQPASDHSPAAEGWVPGSILAPLTATAAESDGS IKKSCSWHTLRMRKRAEVENTGK  
 NEATGPRPKDILGNKVS VKETNSSESECDLDPNTSMEILNPFIQEVAFELVPLVD  
 VTCLLGDTVILQCKVCGRPKPTITWKGPDQNILDTDNSSATYTVSSCDSGEITLKI CNLM  
 PQDSGIYTCIATNDHGTSTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT  
 ISGYTVEYREEGSQIWQQSVASTLD TYLVIEDLSPGCPYQFRVSASNPWGISLPSEPSEF  
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATRKDVAVKFVNKKM  
 KKKEQAHEAALLQHLQHPQYITLHDTYESPTS YILILELMDDGRLLDYL MNHDELMEEK  
 VAFYIRDIMEALQYLHNCRV AHLDIKPENLLIDLRIPVPRVKLIDLEDAVQISGHFHIH  
 LLGNPEFAAPEVIQGIPVSLGTDIWSIGVLT YVMSGVSPFLDESKEETCINVC RVDFS  
 PHEYFCGVSNAARDFINVLQEDFRRRPTAATCLQHPWLQPHNGSYSKIPLDTSRLACFI  
 ERRKHQNDVRPIPNVKSIVNRVNQGT

SEQ ID NO: 165\_5R72\_8\_2\_H  
 MADSGLDKKSTKCPDCSSASQKDVLCVCSSKTRVPPVLV VEMSQTSSIGSAESLISLERK  
 KEKNINRDIRSKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEIIYTFGR  
 ILGKGSFGIVIEATDKETETKWA IKKVNKEKAGSSAVKLLEREVNILKSVKHEHIIHLEQ  
 VFETPKMYLVMELCEDGELKEILDRKGHPSENETRWIIQSLASAIAYLHNNDIVHRDLK  
 LENIMVKSSLIDDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

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## FIGURE 1L

SQOCDIWSIGVVMYMLLRGEPPFLASSEAKLFELIRKGEHFENAVVNSISDCAKSVLKQ  
LMKVDPAHRI TAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEENKPS  
TEEKLKSYQPWGNVPETNYTSDEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE  
IKGEMKTPVTPSQGTATKYPKSGALSRTKKKL

SEQ ID NO: 166\_SGK309\_H  
MQCLAAALKDETMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN  
ALKVESAOQPKQVLKMEVAVLKKLQSGGLGQGDGKEEMMKPGAKRGKDHVCRFIGGRNE  
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSVGLHRDIKPSNF  
AMGRLPSTYRKYMLDFGLARQYTNTTGDVPRPNVAGFRGTVRYASVNAHKNREMRHD  
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMKEKEYEHRMLLKHPSEFHLFLDHIASLDY  
FTKPDYQLIMSVFENSMKERGIAENEFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG  
GQCDASAWGPAPGEHRGCATGRAPEXPECTPNSAREALXGAGPQSPPCPPPRGSXGXSL  
GGDRCQPEQTPDQHRQSNCRQGEGRGWPFLLSPPIPSLVPLPCSSXAPCPPPI SLLARPLF  
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167\_AA234451\_H  
MSGGGEQLDILSVGILVKERWKVLRKIGGGGFGEIYDALDMLTRENVALKVESAOQPKQV  
LKMEVAVLKKLQGDHVCFIGGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR  
LGRQILESIESIHSVGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP  
RAVAGFRGTVRYASINAHNRNEMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE  
RYDHRMLKHLPPFESIFLDHISSLDYFTKPDYQLTSVFDNSIKTFGVIESDPFDWEKT  
GNDGSLTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP  
VGVSPDKLPGLHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL  
GSPIRVRSEITQPRDIPVLRKLRSIHSFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168\_AA435956\_H  
TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIHHQHVLRDLKPQN  
LLISHLGELKLADFGARAKSIPSQTYSSVVTLWYRPPDALLGATEYSSSELDIWAGCI  
FIEMFQGOPLFPVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLH  
VWNRLGRVPEAEDLASQMLKGFPDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV  
RLKPEMCDLLASYQKGHHPAQFSKCW

SEQ ID NO: 169\_AA626859\_H  
NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGI IKICDFGFAQILIPGD  
AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR  
TLGKLI PRHQSI FKSNGFFHGISIPEPEDMETLEEKFSVHPVALNFMKGCLKMNPDRL  
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQONQLLPLIPGSHISPTPDGRKQVLQK  
FDHLPNI

SEQ ID NO: 170\_AA061797\_M  
KIALREIRMLKLKHPNLVNLI EVFRKRKMHVFEYCDHTLLNELERNPNVSDGVKSV  
LWQTLQALNFCHKHNCIHRDVKPENILITKQGM IKICDFGFARILIPGDAYTDYVATRWY  
RAPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLI IRTLKGLI PRHQ  
IFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDRLTCAQLLDSAYF  
ESFQEDQMKRKARSEGRSRRRQONQLLPLIPGSHISPTPDGRKQVVLKFDHLPNI

SEQ ID NO: 171\_AA397553\_H  
MPNSERHGGKKGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHSKHSKMDGLVTPEA  
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSRLHKHRHHQHRRSR

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## FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRI SGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH  
KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDDSSKQDDSPSGA  
SYGQDYDLSPSRHTSSNYDSYKKSPGSTSRQSVSPPYKEPSAYQSSTRSPSPYSRRQR  
SVSPYSKKRSSSYERSGSGSYSGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP  
AYSRHSSSSHSKKRSSSRSRHSSI SPVRLPLNSSLGAELSRKKKRAAAAAAKMDGKES  
KGSPVFLPRKENSSVEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTVEKNSSDTGK  
VKLDENSEKHLVKDLKAQGTRDSKPIALKEEIVTPKETETSEKETPPPLPTIASPPPPPLP  
TTTPPPQTPPLPLPPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSTSAVSSQAN  
SQPPVQVSVKTQVSVTAAI PHLKTSTLPLPLPPLPGGDDMDSPKETLPSKPVKKEKEQ  
RTRHLLTDLPLPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG  
KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPI TAIREIKILRQ  
LIHRSVVNMEIIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLLESGLVHFSEDHIKFSM  
KOLMEGLEYPCHKNFLHRDIKCSNILLNNSGQIKLADFGARLYNSEESRPYTNKVITLW  
YRPPPELLLGEERYTPAIDVWSCGICLGELEFTKKPIFQANLELAQLELISRLCGSPCPAVW  
PDVIKLPYFNTMPKKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCCTAEQTLQSDFL  
KDVELSKMAPDPLPHWQDCHELWSKKRRRQRQSGVVVEPPPSKTSRKETTSGTSTEPVK  
NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSOTDLSIPQMAQLLNI  
HSNPEMQQLEALNQSISALTEATSQQQDSETMAPEESLKEAPSAPVILPSAEQMTLEAS  
STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPQGPRTPTMPQEEAAACPPHIL  
PPEKRPPPPPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPPGHLPEH  
QALRPMEYSTRPRPNRTYGNTDGPETGFSIDTDERNSGPALTESLVQTLVKNRTFSGSL  
SHLGESSYQGTGSVQFPDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVVAETKLQNY  
GELGPGTTGASSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGRGRGVPI

SEQ ID NO: 172\_AA789239\_H  
MEMYETLGKVGEGSYGTVMCKCHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE  
NLVNLIEVFRQKKKIHLVFEFIDHTVLDLQHYCHGLESKRLRKYLFIQLRAIDYLHSNN  
VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVKDTSYG  
KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLVXFMPELKAKLLQEAKVNSLI  
KPKESSENELRKDERKTVYTNLLSSSVLGKEIEKEKKPKEIKVRVIVKVGGRGDI SEP  
KKKEYEGGLGQQDANENVHPMSPDTKLVTIEPPNPINPSTNCNGLKENPHCGGSVTMPPI  
NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSISQVMPNSRQEDPGPIQSQMEKGI  
FNERTGHSDQMANENKRKLNFSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK  
TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173\_AA124976\_M  
LADIVHACLQIDPAERTSSTDLLRHDFYTRDGFIEKFIPELRAKLLQEAKVNSFIKPKEN  
FKENEPVRDEKKSFTNTLLYGNPSLYGKEVDRDKRAKELKVRVIAKGGKGDPDQKKP  
EYEGDHRQOGTADDTQPSLDKKPSVLELTNPLNPSNSDGVKEDPHAGGCMIMPPINLT  
SSNLLAANLSSNLSHPNSRLTERTKKRTSSQTIQOTLSNSRQEDTGPTQVQTEKGAFNE  
RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMVKQIKVLKRESKKTDS  
SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174\_AA575635\_M CCRK\_M  
SASGOLKIADFGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVLDLWAVGCIMG  
ELLNGSPLFP GENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P  
DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP  
GPPHVHDFHVDRIEESLLNPELIRPFIPEG

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## FIGURE 1N

SEQ ID NO: 175\_AA631990\_H  
MITSISTEKSNGTHYPMITTLQYYRGRGGKTAVWRHFS AEGPFAFAEMRHSKRTHCPDW  
DSRESWGHESYRGSHKRKRSHSSTQENRHCKPHHQF KESDCHYLEARSLNERDYRDRRY  
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNHRHCSSHQSRXETV  
DTLGEAFAFGKVV ECI DHGMDGMHVAVKI VKNVGRYREAAARSEIQVLEHLNSTDPNSVFR  
VQMLEWFDHGHGVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHNNKL  
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVVD FGSATYDDEHSTLVSTRH  
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGPIPOHMIQ  
KTRKRKYFHNNQLDWEHSSAGRYVRRRCPLKEFMLCHDEEHEKLFDLVRRMLEYDPTQ  
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176\_AA557536\_H  
MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA  
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG  
LQDVHVRISIFYQLLRATRF LHS GHV VHRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG  
PEDQAVTEYVATRWYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT  
STLHOLELILETI PPPSEEXRPRQTLDALLPPDTSPEALDLLRRLLVFAPDKRLSATQAL  
QHPYVQRFHCPSEDEWAREADVPRPRAHEGVQLSVPEYRSRVYQMI LECGGSSGTSREKGP  
GVSPSQAHLLHKPRADPQLPSRTPVQGP RP RPQSS PGHDP AEHES PRAAKNVPRQNSAPLL  
QTALLNGERPPGAKEAPPLTSLVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV  
RVASVQQVPPRLPPEARPGRRMFSTSALQGAQGGARALLGGYSQAYGTVCHSALGHLPLL  
EGHHV

SEQ ID NO: 177\_N28606\_H, MOK\_H  
MKNYKAIGKIGEGTFSEVMKMQSLRDGNYYACKQMKQRFESIEQVNNLREIQALRRNLPH  
PNILMLHEVVFD RKSGSLALICELMDMNIYELIRGRYPLSEKKIMHYMYQLCKSLDHIH  
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT  
YKMDLWSAGCVFYEIASLQPLFGVNL DQISKIHDVIGTPAQKILTKFKQSRAMNFD  
FKKGSGIPLLTNLSPOCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR  
KAGFPEHPVAPEPLNSCQISKEGRKQKQSLKQEE DRPKRRGPAYVMELPKLKLSGVVRL  
SSYSSPTLQSVLGS GTNGRVPVLRPLKCI PASKKTD PQDLKPAPQQCRLPTIVRKGG

SEQ ID NO: 178\_AB023153\_H, ICK\_H  
MNRYTTIRQLGDGTYSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKNLHA  
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILQGLAFIHLK  
FFHRDLKPENLLCMGP ELVKIADFLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP  
IDVWAVGCIMAEVYTLRPLFGASEIDTIFKICQVLGTPKKTWDWPEGYQLSSAMNFRWPQ  
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS  
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQHQASQPPLHLTPYKA EVSRTDH  
PSHLQEDKPSPLLFPSLHNKHPQSKITAGLEHNKEIKPKSRRRWGLISRSTKDSDDWAD  
LDDLDFSPSLSRIDLKNNKRSDDTL CRFESVLDLKPSEPVGTGNSAPTQTSYQRRDPT  
LRSAAQHLYLKHRYLPGISIRNGILSNPGKEFIPNPWSSSGLSGKSSGTMSVISKVNS  
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPIPDPSPGYSSLKAMRPHPGRPFLDT  
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179\_AA839940\_M  
SSNNGGMSAEEIIGPGAEPMRGPSLATRDWRDET VGT TDLQQGIDPGAVSPEPGKDHAHQ  
GPGRTEAGRVSSAAEAAIVLDDSAAPPFEHRVVS IKDTLISAGYTVSQHEVLGGGRF  
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLILQLYDAFESKNSFT  
LIMEYVDGGELFDRI TDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

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## FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL  
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSATQCLK  
HEWLNHLPAKASGSNVRLRSQQLLOKYMAQSKWKHFHVVAVNRLRKFTPCTP

SEQ ID NO: 180\_AA460132\_H

MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGAAVIK  
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVFFVDYASNCLYMEEIEGSV  
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
LIDFGLSFISALPEDKGVLDLYVLEKAFLLSTHPNTETVFEAFKSYSTSSKKARPVLKKLD  
EVRLRGRKRSMVG

SEQ ID NO: 181\_SGK034\_H

QREKVNQGNMPLQSTFLAMDTTEGVEVVWNLHFGRKAFAAHEEKIQTTFEQLVLVDH  
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKTKKNHKAMNARAWKRWCTQILS  
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVVHRIFSNAIPDDLRSPIRAEREELR  
NLHFFPPEYGEVADGTAVDIFSFGMCALEMAVLEIQTNQDTRVTEEAIAARARHSLSDPNM  
REFILCCLARDPARRPSAHSLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAM  
DLHAVLAELPRPRPPLQWRYSEVSFMELEDFVDRNGIYPLMNFAATRPLGLPRVLAP  
PPEEVQAKTPTPEPFDSETRKVIQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLL  
PTDSAQDLASELVHYGFLHEDDRMKLAFLSTFLKYRGTOA

SEQ ID NO: 182\_AA103218\_M SGK034\_M

HASAPYGEVNDGTGFVDIFSFGMCALEMAVLEIQANGDTRVTEEAIAARARHSLSDPNMR  
EFILSCLARDPARRPSAHNLLFHRVLFVHSLKLLAAHCFIQHQYLMPEENVVEEKTAMD  
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVDRNGIYPLMNFAAARPLGLPRVLAP  
PEEAQKAKTPTPEPFDSETRKVVQMCNLERSEDKARWHLTLLLVLEDRLHRQLTYDLLP  
TDSAQDLAAELVHYGFLHEDDRTKLAFLSTFLKYRGTOA

SEQ ID NO: 183\_NEK7\_H, N34132\_H

MSGGAAEQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT  
MDKDSRGAAATTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH  
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSPQSLVGSKEEPP  
ARSGSGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVYKGLD  
TETTVEVAWCELQDRKLTKEQRFKEEAEMKGLQHPNIVRFYDSWESTVKGKCCIVLV  
TELMTSGTLKTYLKRFKVMKIKVLRSWCRQILKGLQFLHTRTPLIIHRDLKCDNIFITGP  
TGSVKIGDLGLATLKRASFASVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY  
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIEGCIQONKDERYSIKDLLNHAFQ  
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGYKDNEAIEFCFDLERDVPEDVAQEM  
VESGYVCEGDHKTMAKAIKDRVSLIKRKEQRQLVREEQENKKQEESLKKQVEQSSASQ  
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLOQQPSISVLSGDTVDSGQG  
SSVFTESRVSSQQTVSYGFPXHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVQQGIQQ  
TAPPQQTQVQYSLSQTSSEATTAQPVSPQAPQVLPQVSAGKQSTQGVSVQVAPAEVAV  
AQPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSRHEGRTTKRHYRKSRSRHE  
KTSRPKLRILNVSNKGRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFILAE  
RESFVDQVREIEKADEMLSEDVSVEPEGDQGLSLOGKDDYGFSGSQKLEGEFKQPIPA  
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN  
LSHSASSLSLQQAQFSELRAQMTEGPNTAPPNFSHTGPTFPVPPFLSSIAGVPTTAAAT  
APVPATSSPPNDISTSVIQSEVTVPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSV  
SSITIPAVVISITTSPLQVPTSTSEIVSSTALYPSVTVSATSASAGGSTATPGPKPPA  
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

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## FIGURE 1P

HSSTTGLAFSLAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL  
 LPQVPSIPPLVQPVANVPAVQQTLIHSQPPALLPNQPHTHCPEVDSDTQPKAPGIDDIK  
 TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP  
 TNLPLGTVALPVTVPVTPGQVSTFVSTTTSGVKPGTAPSKPPLTKAPVLPVGTETLPA  
 PSEQLPPFPGPSLTQSQQPLEDLDAQLRRTLSPMITVTSVAVGPVSMAPTAITEAGTQP  
 QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTESS  
 VLSSSSPESTLVKPEPNGITIPGISSDVPESAHTTASEAKSDTGQPTKVGRFQVTTAN  
 KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVLPKKEKPELSEPSHLNGPSSD  
 PEAFLSRDVEDDGSGLSPHSPHQLSSKSLPSQNLSSQSLNSFNSSSYMSSDNESDIEDDLK  
 LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVPVAVIIPPAAPLSGRRRRPTKSKGS  
 KSSRSSSLGNKSPQLSGNLSSQSAASVLHPQQTLPHPGNIPEGQNLQLPLKPSPSDN  
 LYSFTSDGAISVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184\_BCON3\_H  
 MSEGESQTVLSSGSDPKVSSSSAPGLTSVSPVSTTSAASPEEEEESEDESEILEESP  
 CGRWQKRREEVNQRNVPIDISAYLAMDTTEGVEVWNEVQFSEKKNYKLQEEKVRVFDN  
 LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSSGSLKQFLKKTCKNHNKTMNEKAWKRW  
 CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHNKTCREEQKNL  
 HFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNGESSYVPQEAISSAIQLLEDPLQ  
 REFIOKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMIPENALEEITKNM  
 DTSVLAIEIPAGPGREPVTLYSQQPALELDKFLEDVRNGIYPLTAFGLPRPQQQEEV  
 TSPVPPSVKTPTEPAEVEVTRKVVLMQCNIESVEEGVKHHLTLLKLEDKLNRLSCDL  
 MPNENIPELAELVQLGFISEADQSRLTSLLEETLNKFNFNSTLNAAVTSS

SEQ ID NO: 185\_AA711829\_M  
 LKQFLKKTCKNHNKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK  
 IGSVAPDTINNHNKTCREEQKNLHFFAPEYGEVTNVTAVDIYSFGMCALEMAVLEIQNG  
 GESSYVPQEAISSAIQLLEDPLQREFIOKCLQSEPARRPTARELLFHPALFEVPSLKLAA  
 AHCIVGHQHMIPENALEEITKNMDTSVLAIEIPAGPGREPVTLYSQQPALELDKFLEDV  
 RNGIYPLTAFGLPRPQQQEEVTSPPVPPSVKTPTEPAEVEVTRKVVLMQCNIESVEEG  
 VKHHLTLLKLEDKLNRLSCDLMPNENIPELAELVQLGFISEADQSRLTSLLEETLNK  
 FNFTRNSTLTATVTSS

SEQ ID NO: 186\_AA099102\_H  
 MSSCVSSQSSNRAAPQDELGGGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP  
 GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR  
 CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGSYGVVK  
 LAYNENDNTYYAMKVLSSKKLIRQAAPRRPPRGRTRPAPGGCIQPRGPIEQVYQEIAIL  
 KKLDPNVVVLVEVLDDPNEDHLYMVFEVNVQGPVMEVPTLKLSEDQARFYFDLIKGI  
 EYLHYQKIHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTAFMAPESLS  
 ETRKIFSGKADVWAMGVTLVCFVFGQCPFMDERIMCLHSKIKSQALEFPDQPDIAEDLK  
 DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPPLPSEDENCTLVEVTEEEVENSVKHIPS  
 LATVILVKTMRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP  
 PGRHPAPRGGSALVRGSPCVESWAPAGSPARMHPLRPEEAMEPE

SEQ ID NO: 187\_5R69\_17\_2\_H  
 MQEIPQEQIKEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR  
 QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGTRELLDREKDLTLG

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## FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSMSLGTT  
REKTDREVSTAYLSPQELEDFYQYDVKSEIYSFGIVLWEIATGDI PFQGEEDWLSQW  
L

SEQ ID NO: 188\_H85811\_H

MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS  
QPATTTVSTSLPVPNPSPYEQTI VFPGSTGHIVVTSASSTSVTGQVLGGPHNLMRRSTV  
SLLDTYQKCGLRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS  
EGDYQLVQHEVLCMTNTYEVLEFLGRGTGQVVKCWKRGTNEIVAIKILKNHPSYARQG  
QIEVSILARLSTESADDYNFVRAYECFQHKHNTCLVFEMLEQNLDFLKQNKFSPLPLKY  
IRPVLLQVATAMKLSGLIHADLKPENIMLVDPSPRQPYRVKVIDFGSASHVSKAVCST  
YLSRYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP  
AEYLLSAGTKTTRFFNRDTSPLYLWRLKTPDDHEAETGKSKARKYIFNCLDDMAQVN  
MTTDLGSDMLVEKADRRFIDLLKMLTIDADKRITPIETLNHPFVMTTHLLDFPHSTH  
VKSCFQNMIECKRRVNMVDTVNQSKTPFI THVAPSTSTNLMTFNNQLTTVHNQPSAASM  
AAVAQRSMPLQTGTAQICARPDFFQQAALIVCPGFGQLQASPSKHAGYSVRMENAVPIVT  
QAPGAQPLQIQPGLLAQQA WPSGTQQIILLPPAWQQLTG VATHTSVQHATVIPETMAGTQQ  
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAPLNVGVAVHMRQQPTSTSSRKSKQH  
QSSVRNVSTCEVSSSQAISSPQSRKRVKENTPPRCAMVHSSPACSTSVTCGWGDVASSTT  
RERQRTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPLS  
DSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDLSL  
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITRQQRPGPHFQQQQPLNLSQAQQHI  
TTDRGTGSHRRQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAHLPTQPHLYTYTA  
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQPVPVSMGPRVLPSTIHP SQYPAQF  
AHQTYISASPASTVYTYGYP LSPAKVNQYPYI

SEQ ID NO: 189\_DYRK3\_H

MMIDETKCPPCSNVLCNPSEPPPPRRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR  
KSNTIQSDGISDSEKCSPTVSQKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT  
AYEKL E I INYPEIYFVGPNAKKRHGVIGGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII  
GKGSFGQVARVYDHKL RQYVALKMVRNEKRFHRQAEEIRILEHLKKQDKTGSMNVIHML  
ESFTFRNHVCMAFELLSIDLYELIKKNKFQGF SVQLVRKFAQSILQSLDALHKNKIIHCD  
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF  
RCILAE LLTGQPLFPGEDEGDQLACMELLGMPPPKLLEQSKRAKYFINSKGI PRYCSVT  
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDYLFIEFLKRC LHWDP SARLTPAQ  
ALRHPWISKSVPRPLTTIDKVSGKRVVNPASAFQGLGSKLPPVVGIANKLKANLMSETNG  
SIPLC SVLPKLIS

SEQ ID NO: 190\_AA589241\_M DYRK3\_M

TRPELLGMPPQKLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVVLGGRSRRGKKRGPPG  
SKDWATALKGCGDYLFIEFLKRC LQWDPSARLTPAQALRHPWISKSTPKPLTMDKVPGKR  
VVNPTNAFQGLGSKLPPVVGIA SKLKANLMSETSGSIPLC SVLPKLIS

SEQ ID NO: 191\_5R72\_16\_2\_H

MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLY  
PQGLTGEEVYVKVLDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE  
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQORLLEAKRKEEQEQRILHEIQ  
RRKEEIKEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAI LHGGSPDFVGNKGHR  
ANSSGRSRRERQYSVCNSEDSPGSC EILYFNMGSPDQLMVHKGKIGSDEQLGKL VYNAL  
ETATGGFVLLYEWVLQWQKMGPF LT SQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVR

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## FIGURE 1R

YLAMNLKEQDDSIIVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLSNS  
 VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD  
 VWRLGLLLLSLSQGECEYPTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN  
 PQPKMPLVEQSPEDSGGQDYVETVIPSRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA  
 FGAVIKVQNKLDGCCYAVKRIPIPNASRQFRRIKGEVTLLSRLHHENIVRYNAWIERHE  
 RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVEWSTSGERSAS  
 ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSEDIIFDNEDENSKSQNQDEDCNEK  
 NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH  
 EKGMIHRDLKPVNIFLSDDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG  
 MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPSTP  
 KFPEDFDDGEHAKQKSVISWLLNHPAKRPTATELLKSELLPPPQMEESSELHEVLHHTLT  
 NVDGKAYRTMMAQIFSQRISPAIDYTYDSILKGNFSIRTAKMQQHVCETIIRIFKRHGA  
 VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE  
 RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIITYIYEIIQEFPAQERNYSIYL  
 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSNSLCRLYKF  
 IEQKGLDQDLMPNTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYK  
 VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDILLIPQFRGPQALGPVPTAIGVSIADK  
 ISAAVLNMEESVTISSCDLLVSVGQMSMRINLTQKLWTAGITAEIMYDWSQSQEELQ  
 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETTELVDHVLQKLRTKVTDERNG  
 REASDNLAVQNLKGSFNSASGLFEIHGATVVPVSVLAPEKLSASTRRRYETQVQTRLQT  
 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC  
 DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192\_R43524\_H, HRI\_H  
 MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQOQTFP  
 FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSFTCSDEFSSRLHH  
 NRAITHLMRSKERVQDPCEDISRIQKIRSREVALEAQTSTRYLNEFEELVILGKGGYGR  
 VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHI  
 QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSIIFAEPTPEKEKRFGESDTENQ  
 NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQLPLRRNSHLEESFTSTEE  
 SSEENVNFLGQTEAQYHMLHIQMLCELSDLWDWIVERNKRGREYVDESACPYVMANVAT  
 KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN  
 GKRTPTHTSRVGTCLYASPEQLEGSEYDAKSDMYSLGVVLELFPQFGTEMERAEVLTGL  
 RTGQLPESLRKRCVPQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLMKII EQ  
 EKEIAELKKQLNLLSQDKGVRDDGKDGCVG

SEQ ID NO: 193\_17000057519457\_H  
 MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK  
 HRFPGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVFFVDYASNCLYMEEIEGVS  
 TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
 LIDFGLSFISALPEDKGVLDYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD  
 EVRLRGRKRSMVG

SEQ ID NO: 194\_AA013524\_M  
 LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRRTVQEARALLRCRRAGIA  
 APVFFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAMHDQD  
 LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFVSGLPEDKGVLDYVLEKAFLSTHPHTETA  
 FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

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## FIGURE 1S

SEQ ID NO: 195\_17000139801197\_H, IRAKM\_H  
MAGNCGARGALSAHTLLFDLPPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK  
YVDQKSGTREL LWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG  
FPNILFKETANVTVDNVLIPHENEKGVLLKSSISFQNTIEGTRNFHKDFLIGEGEIFEVY  
RVEIQNLTYAVKLFKQEKMQCKKHWRFLSELEVL L LFHHPNILELAAYFTETEKFC LI  
YPMRNGTLFDR LQCVGDTAPLPWHIRIGILIGISKAIHYLHNVPQCSVICGSISSANIL  
LDDQFQPKLTDFA MAHFRSHLEHQ SCTINMTSSSSKHLWYMPEEYIRQ GKLSIKTDVYSF  
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRG L DSCLSFLDKKVP PCPRNFS AKLFC  
LAGRCAATRAKLRPSMDEV LNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE  
DDESQNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSSCE  
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196\_AA840598\_M IRAKM\_M  
MWKRFLSELEVL L LFRHPHILELAAYFTETEKLC LVYPYMSNGTLFDR LQCTNGTTPLSW  
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANIL LDDQLQPKLTDFAAAHFRPNLEQQ  
SSTINMTGGGRKHLWYMPEEYIRQGR LSVKTDVYSFGIVIMEVLTGCKVVLDDPKHVQLR  
DLLMELMEKRG L DSCLSFLDRKIPPCPRNFS AKLFLAGRCVATKAKLRPTMDEV LSSLE  
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNH SVPPKEVLGTDRVTQK  
TPFECSQSEVTF LGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGSS  
WEVPGHSYGSKPMEKRCSSGLFCSEHEQSKKO

SEQ ID NO: 197\_AA088547\_H  
MASAVRGSRPWPRLGLQLQFAALLGLT LSPQVHTLRPEN L L LVSTLDGSLHALSKQTGDL  
KWTLRDDPVI EGP MYVTEMAFLSDPADGSLYILGTQKQQLMKLPFTIPELVHASPCRSS  
DGVFYTG RKQDAWFVDPESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDPAPALRWNT  
TYRRYSAPPMDGSPGKYM SHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL  
RQLPHLT LARDTLHFLALRWGHIRLPASGPRDTATLFSTLDTQLMTLYVGKDETGFYVS  
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPGSGVALPSQWLLI  
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK  
TPDSYLGLGPQDLLAASLTAVLLGGWILFVMRQVVEKQQETPLAPADFAHISQDAQSLHS  
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGT FVFRGQFEGRA  
VAVKRL LRECFGLVRREVQLLQESDRHPNV LRYFCTERGPOFHYIALELCRASLQEYVEN  
PDLDRGGLEPEVVLQQLMSG LAHLHSLHIVHRDLKPGNILITGPD SQGLGRVVLSDFGLC  
KKLPAGRCFSLSHSGIPGTEGWMAPELLQLLPDSPTS AVDIFSAGCVFYVLSGGSHPF  
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR  
AKQLQFFQDVSDWLEKESEQEPLVRALEAGGCAVVRDNWHEHISMP LQTDLRKFRSYKGT  
SVRDLLRAVRNKKHHYREL PVEVRQALGQVPDGFVQYFTNRFPRL L L LHTHRAMRSCASES  
LFLPYYPDSEARRPCPGATGR

SEQ ID NO: 198\_HGP\_6644466  
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRS PRGLSHSP  
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE  
KSLNDLIEERYKASQDPFPAAILKVALNMARG L KYLHQEKLLHGDIKSSNVVIKGD FE  
TIKICDVGVS LPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM  
MTLSIPHINLSNDDDDDEKTFDESDFDDEAYYAALGTRPPINMEELDES YQKVIELFSVC  
TNEDPKDRPSAAHIVEALET DV

SEQ ID NO: 199\_AA449542\_M  
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKNLNHPNIIGYRAFTEASD GSL  
CLAMEYGGEKSLNDLIEERNKDSGSPFPAAVILRVALHMARG L KYLHQEKLLHGDIKSS



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## FIGURE 1T

NVVIKGFETIKIKCDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV  
AFGLTLWEMMTLCIPHVNLPDDDDVEDATFDESDFDEAYYAALGTRPSINMELDDSYQK  
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200\_5R57\_10\_2\_M TESK2\_M  
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201\_AA232253\_H  
MSSLGASFVQIKFDDLQFFENC GGSGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL  
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMHIMTWATDVAKMHY  
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFPWWAPEVIQS  
LPVSETCDTYSYGVVLWEMLTREVFPFKGLEGLQVAVLVVEKNERLTIPSSCPRSFAELLH  
QCWEADAKKRPSFKQIIISILEMSNDTSLPDKNSFLHNKAWEKCEIEATLERLKKLERD  
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE  
MSVYASLFKENNITGKRLLLLEEDLDKMGIVSKGHIHFKSAIEKLTHDYINLFHFPPL  
IKDSGGEPEENEKIVNLELVFGFHLKPGTGPDCKWKMYMEMDGEIAITYIKDVTFTNT  
NLPDAEILKMTKPPFVMEKWIIVGIAKSQTVECTVTYESDVRTPKSTKHVHLIQWSRTKPQ  
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADQWLDTLRMRQIASNTSLQRSQSNPILGSP  
FFSHFDGQDSYAAAVRRPQVPIKYQOITPVNQSRSSSPTQYGLTKNFSSHLNSRDSGFS  
SGNTDTSSERGRYSDRSRNKYGRGSI SLNSSPRGRYSGKSQHSSTPSRGRYPGKFYRVSQS  
ALNPHQSPDFKRSPRDLHQPNTPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP  
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202\_AI375137\_H  
MGNYKSRPTQTCTDEWKKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL  
NYRTENGLSLLHLCCICGGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL  
LHSGADIQQVGYGGLTALHIATIAHGLEAADVLLQHGANVNIQDAVFFTPLHIAAAYYGHE  
QVTRLLLKFADVNVSSEVGDRLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVP LH  
FCSRFGHHDIVKYLLQSDLEVQPHVNIYGDTPHLHLACYNGKFEVAKI IQISGTESLTK  
ENIFSETAFHSACTYGKSIDLVKFLLDQNVININHQRDGTGLHSACYHGHIRLVQFL  
DNGADMNVLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG  
GDGSYVSVSPPLGKIKSMTKEKADILLRAGLPSHFHLQLSEIEFHEI I GSGSFGKVYKG  
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLNDP SQFAIVTQ  
YISGGSLSLLEQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG  
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT  
GEIPFAHLKPAAAAAD MAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE  
ECLCNIELMSPASSNSSGSLSPSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA  
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSRNSSSFEDSS

SEQ ID NO: 203\_H97685\_H  
MESERSPLYRQLIDLGYLSSSHWNC GAPGQDTKAQSMLEQSEKLRHLSTFSSHQVLQTRL  
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE  
MKMDIVETLNTMKEELLDDATNMEFKDVI VPENGEVGTREIKCCIRQIQELIISRLNQA  
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQILNAAHYHEVTFHSGS  
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS  
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHPRLARLSLESRSLODVLHHRKPKLG  
QELGRGQYGVVYLCDNWGGHFPALKSVVPDEKHWNDLA LEFHYMRSLPKHERLVDLHG  
SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH  
RDIKLNVLDDKQNRAKITDLGFCCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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## FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK  
RPLLGVQPMLOQIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204\_W20810\_M

DVNLKASKASDVYSFGILVWAVLAGREAEVLVDKTSILIRETVCDRQSRPPLTELPPGSPET  
PGLEKLKELMIHCWGSQSENRPSPQDCEPKTNEVYNLVKDKVDAAVSEVKHYLSQHRSSG  
RNLSAREPSQRGTEMDCPRETMVSKMLDRLHLEEPSGPVPGKCPERQAQDTSVGPATPAR  
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQORNQGDGRHGTWPYPWTPPNPMTGP  
PALVFNNCSEVQIGNYNLSLAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205\_AA744236\_H

MGSSENSALKSYTLREPPFTLPSGLAVYPVAVLQDGKFASVFVYKRENEDKVNKAACHLKTLL  
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALIFLHDRGHL  
THNNVCLSSVFSVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPPEEMSPEFTT  
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSFQOTLHSTLLNPIPKCRPALCTLL  
SHDFFRNDLFLEVNFLLKSLTLKSEEEKTEFFKFLLDVRSCLSEELIASRLVPLLLNQLVF  
AEPVAVKSFPLPYLLGPKKDHAGGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLSSH  
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI  
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSSENFPSSSKKSEEWPDWSE  
PEEPENQTVNIQIWPREPCCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV  
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG  
LGEEFTIQVKKKPVKDPMDWFAFMIPEIKPSAAFLILPELRTMVPKKDDVSPVMQFSS  
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206\_AI052250\_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE  
VAVFVFDKKLIDKYQKFEKDQIIDSLKRGVQQLTRLRHPRLTLVQHPLEESRDCLAFCTE  
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT  
PENIILNKSGAWKIMGFDVCSSTNPSEQEPKFPCKEWDPNLPSLCLPNPEYLAPEYILS  
VSCETASDMYSLGTVMYAVFNKGKPIFEVVKQDIYKFSRQLDQLSRLGSSSLTNIPEEV  
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAFTLQYFDTLQFQDNLQKSQFFKGLPKVL  
PKLPKRIVIVQRIPLCLTSEFVNPDMPVFPVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ  
EPIQILLIFLQKMDLLLTCTPPDEIKNSVLPMVYRALEAPSIQIQELCLNIIPTFANLID  
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207\_AA278842\_H

MWFFARDPVRDFPFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV  
AKAAFKRFTLRHPNILAYIDGLETEKCLHVTEAVTPLGIYLKARVEAGGLKELEISWG  
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQNGGGGPPRKGIPE  
LEQYDPPPELADSSGRVREKWSADMWRLGCLIWEVFNGPLPRAAALRNPGKIPKTLVPHY  
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS  
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVKMFSS  
TDRAMRIRLLQOMEQFIQYLDEPTVNTQIFPHVVHGFLLDTNPAREQTVKSMLLLAPKLN  
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF  
APSRVAGVLGFAATHNLYSMNDCAQKILPVLGCLTVDPKSVRDQAFKAIRSFLSKLESV  
SEDPTQLEEVEKDVHAASSPGMGGAASWAGWAVTGVSSTLSKLIRSHPTTAPTETNIPQ  
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDEDWGSLEQEAESVL  
AQDDWSTGGQVSRASQVNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEPDPGTR  
LASEYNWGGPESDCKGDPFATLSARPSTQPRPDSWGEDNWEGLTDSRQVKAELARKRE  
ERRREMEAKRAERKVAKGPMKLGARKLD

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## FIGURE IV

SEQ ID NO: 208\_AA599286\_H  
MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD  
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD  
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLWS  
ADLGPDKYLSKDFQCLIKLLPSC LHPYIYRVTFATANESSALLIRMFNEKGTLDLIYK  
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFYPYGHLLHASNVMLDGD  
CRLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP  
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPFLSDVLLTTSEKPQFKIPTKLKEALR  
IAKECIEKRLIEEQKQIHQHRRLTRAQSHHGSEERKKRILARKKSKRSALENSEEHS  
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEAPAQLS  
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSSAEASCLHLEGKVLFFYSYSPLPN  
YPLPGKVIAPVQPPQTVLFCRCSCQKLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209\_AA425725\_H  
MSASTGGGGDSGGSGSSSSQASCGPESGSELALATPVPQMLQGLLGSDDDEEQEDPKD  
YCKGGYHPVKIGDVFNGRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVVSAGHYTETA  
VDEIKLLKCVRDSDPSPDKRETIVQLIDDFRISGVNGVHVCMLVLEVLGHQLLKWIIKSNY  
QGLPVPCVKSIVRQVLHGLDYLHTCKCKIHTDIKPENILLCVGDAYIRRLAAEATEWQQA  
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRLDLQRLAMEAATQA  
EDSGLRLDGGSGSTSSSGFSGSLFSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP  
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEGPPADIWSTACMAF  
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDIPPAFALSGRYSREFFNRRGELRHIHN  
LKHGGLYEVLMKEYEWPLEQATQFSAFLLPMEYIPEKRASAADCLQHPWLN

SEQ ID NO: 210\_SGK022\_H  
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKICLVMELAEGGDVFDVNLGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCNALLQGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLSISADCQD  
LLKRLLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211\_AA060026\_M SGK022\_M  
MEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKIIDKMGGPEEFIQRFLPRELQ  
IVRTL DHKNI IQVYEMLESADGKIYLMELAEGGDVFDVNLGGPLPESRAKALFROMVE  
AIRYCHGCGVAHRDLKCNALLQGFNLKLTDFGFAKVLPKSRRELSQTFCGSTAYAAPEV  
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLGISTECQD  
LLKRLLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212\_AA399669\_H  
MGKGDVLEAAPTTTTAYHSLMDEYGYEVGKAIGHGSYGSVYEFYTKQKVMVAVKIISSKK  
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA  
CSEPLAGKWFSQTLGIAYLHKSIVHRDLKLENLLLDKENVKISDFGFAKMVP SNQPV  
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVV AHLPF  
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213\_AA758539\_H  
MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE  
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLLFIKCGALHEDVARKMFRQL  
SSAVKYCHDLDIVHRDLKCNLLLDKDFNIIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

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FIGURE 1W

YAAPEVLQSI PYQPKVYDIWSLGVILYIMVCGSMPLYDDSDIRKMLRIQKEHRVDFPRSKN  
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD  
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMDRLAETSRKDHHS GAIEVKGAST

SEQ ID NO: 214\_AA883975\_H  
MSGDKLLSELGYKLGRITIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE  
LSILRGVRHPHIVHVFIEFIEVCNGKLYIVMEAAATDLLQAVQNRGRI PGVQARDLFAQIA  
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSSTTYCGSAAAYASP  
EVLGIPYDPKPYDVWSMGVLYVMVTGCMFDDSDIAGLPRRQKRGVLYPEGLELSERC  
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215\_AA905446\_H  
VGRQETGVRRWAFLICQIPSPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG  
KICLVMELAEGGDVDFCVLNGGGLPESRAKALFROMVEAIRYCHGCGVAHRDLKCENALL  
QGFNLKLTDFGFAKVLPKSHRELSQTFCGSTAYAAPEVLQGI PXKMLWQQQKGVSFPTH  
SISADCQDLLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 216\_H29974\_H  
YSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV  
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFMFCEGG  
DLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD  
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG  
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG  
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217\_AA498104\_M H29974\_M  
PLLLPPPPAAMETGKENGARRGTS PERKRRSPVQORVLC EKL RPAAQAMPAGAEVPGEA  
FLARRRPDGGGDV PARPRYSLLAEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE  
LALAEFWALTSLKRRHQNI VQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL  
GYAEPCYLWFMFMEYCEGGDLNQYVLSRRPD PATNKSFMLQLTSAIAFLHKNHIVHRDLK  
PDNILITERSGTPILKVAD FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM  
APEVWEGHYTAKADIFALG II IWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE  
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218\_AA215311\_H  
MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI  
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPR SAYYLWFMVD  
FCDGGDMNEYLLSRKPNRKTNTS FMLQLSSALAF LHKNI IHRDLKPDNILISQTRLDTS  
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTFYMAPEVWEGHYTAKADI  
FALG II IWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM  
NGRMKQLIKEMLAANPQDRPD AFELELRLVQIAFKDSSWET

SEQ ID NO: 219\_AA018361\_H  
MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT  
ERLGS GTYATVYKAYAKKDTREVVAIKCVAKKSLNKASVENLLTEIETLKGIRHPHIVQL  
KDFQWSDNIY LIMEFCAGGDLSRFIHTRILPEKVARVFMQQLASALQFLHERNISHLD  
LKPQNILLSSLEKPHLKLADFGFAQHMSPWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW  
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR  
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALS LYCKALDFFVPA

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## FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKPRLL  
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSRAGGGSCFTLRFRTSWPELN  
T

SEQ ID NO: 220\_AA311714\_H  
MENFILIYEEIGRGSKTUVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT  
FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL  
KFSNFCLAKVEGENLEEFFALVAAEEGGGDNGENVLKKSMSRVKGSVPVYTAPEVVRGAD  
FSISSDLWSLGLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN  
LLDGLLQRDPQKRLTWTRLLQHSFWKKAFAQADQESSVEDLSLSRNTMECSGPQDSKELL  
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV  
SPGEDMTHCSPOKTSPLTKITSGHLSQQDLESQMRELIYTDSDLVVTPIIDNPKIMQPP  
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV  
AGHQEVATRLHSPFLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS  
SIGIGILNCLVQHSTPVPRQCLVYV

SEQ ID NO: 221\_SGK384\_H  
SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCLHR

SEQ ID NO: 222\_AA210451\_M SGK384\_M  
MQQQHGRTRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPPGYFR  
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH  
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLKYQDVNTWQHRLQL  
AMEYVSIINYLHHSPLGTRVMCDSDNLPKTLQYLLTSNFSIVANDLDALPLVDHDSGV  
IKCGHRELHGDFVAPEQLWPYGEDTFFQDDLMPSYNEKVDIWKIPDVSSFLGHVEGSDM  
VRFHLDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223\_SGK071\_2\_H  
EUVAVQMMVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF  
NELSFQEVIEDKRKAKKIIDSEWMQNVGLQVLDALLEYLHHLDIHRNLKPSNIILISSDH  
CKLQDLSSNVMLTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC  
SFMDOGTEAMHLRKSRLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD  
VWHITFLRGSFKSSCVSLTLHRQMPASITDMLLEGNVASILGDAGDTKGERALKLLSMA  
LASYCLVPEGSFLMPLALLHMHQWLSCDQDRVPGKRDFAVLGKLGLLGPPIPKGLPWPP  
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH  
PEEEPLLVMVYSLLAITTTQESSESLSEELQNAAGLLEHILEHLNSSLERSDVCASGLGLLW  
ALLLDDPILALQRPKRKRPNHKGPKPKNPASTQSIIVNKAPLEKVPDLISQVLATYPA  
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIIRLCQDRALLVNNAYRGLASLVKV  
SELAFAFKVVVQEEGGSLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM  
KALLQEIKERFTSSSLVSDSSAFSKPGLPPGSPQLGCTTSGGLE

SEQ ID NO: 224\_AA118352\_M SGK071\_M  
EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL  
KPILKTMEEKQIPGTDVYLLLPFMLHINPSDLRAIKDVMQVTFMSNSFKSSVALNMQR  
QKVPIFITDVLLGNNMANILGSWLCASFVNSRHCDSGIGSQRLGFDQSVSWTEHPLKD  
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEVISI IKQHGRILDILLSTCSLL  
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQQISEEL  
EEGLFQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP  
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLSIQLCPGRVLLVNNAFRGLASLAK

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## FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG  
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGQLQEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225\_018653.9\_H

GRGRGAGHARGLRGPAGRAEPPRSLSRPGPGPSRAGPAGRGEESDAAPAGGSGRGFL  
RLLPAGLRPQALRSGSEPPRPGQSPEPSPAPGAGRRGGRGELARQIRARYEEVQRYSRG  
GPGPGAGRPERRRLMDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA  
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA  
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTSWEDRF  
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI  
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDIVNATGE  
LAWGVDETALQLEKVLHLYRSGQYLQNSTASSSTEYQCI PDSTIPQEDYRCWPSYHHGSC  
LLSVFNLAEAVDVCESHAQCRAFVVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226\_AA396601\_M

TRPGCAALRNVSGAQYVSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG  
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEIPDTLTTITELGAPVEMIQLLQTSWEDRF  
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPC  
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDIVNATGE  
LAWGVDETALQLEKVLHLYRSGQYLQNSTASSSTEYQRI PDSAITQEDYRCWPSY  
HHGCLLSVFNLAEAIDVCESHAQCRAFVVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY  
VKAPG

SEQ ID NO: 227\_VRK3\_H

MISFCPDCGKSIQA AFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP  
KKVKWSSTVTS PRLSLFSGDSSSEEDTLSSSERSKSGSRPPTPKSSPQKTRKSPQVTR  
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLSFQTRDNQGIL  
YEAAPTSTLTCDSGPQKQKFSKLDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA  
IPTCMGFGVHQDKYRFLVLP SLGRSLQSLADVSPKHVLSERSVLQVACRLLDALEFLHEN  
EYVHGNVTAENIFVDPEDQSQVTLAGYGFAFRYCPSGKHVAYVEGSRSPHEGDLEFI SMD  
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGPCCGH  
WIRPSETLQKYLKVVMA LTYEEKPPYAMLRNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228\_S71575\_M VRK3\_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSLADDDNPKHVVSERCVLQVACRLLDALEYLHEN  
EYVHGNLTAENVFVN PEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFI SMD  
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR  
WNKASETLREYLKVVMA LNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQMPV

SEQ ID NO: 229\_AA45427\_H

MGHALCVCSRGTVIIDNKRYLFIQKLGE GGF SYVDLVEGLHDGHFYALKRILCHEQQDRE  
EAQREADMHRLFNHPNIRLVAYCLRERGAKHEAWLLLPFFKRGTLWNEIERLKDKNFL  
TEDQILWLLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLM DLGSMNQACIHVEGS  
RQALTQDWAQRC TISYRAPELFSVQSHCVIDERTDVWSLGC VLYAMMFEGEPYDMVFQ  
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRP H I PLLSQLEALQPPAPGQ  
HTTQI

SEQ ID NO: 230\_H05721\_H

MAVRQALGRGLQLGRALLRFTGKPGRAYGLRPGPAAGCVRGERPGWAAGPGAEP RRVG  
LGLPNRLRFFRQSVAGLAARLQRQFVVRAGWCAGPCGRAVFLAFGLGLGLIEEKQAESRR

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## FIGURE 1Z

AVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIQSIGKGCSAAVYEATMPTLPQ  
NLEVTKSTGLLPGRPGTSAPEGQERAPGAPFPLAIKMMWNI SAGSSSEAILNTMSQE  
LVPASRVALAGEYGAVTYRKS KRGPQLAPHPNI IRVLRAFTSSVPLLP GALVDYDPVLP  
SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQ LLEGVDHLVQGGIAH  
RDLKSDNILVELDPDGC PWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVST  
ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGQGAHLESRSYQEAQLPALPESVPP  
DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQAATLL  
ANRLTEKCCVETKMMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231\_AI086865\_H  
MEKYERIRVVGRAFGIVHLCLRKADQKLVIKQIPVEQMTKEERQAAQNECQVLKLLNH  
PNVIEYYENFLEDKALMIAMEYAPGGT LAEFIQKRCNSLLEEETILHFFVQIILLALHHVH  
THLILHRDLKTQNILDKHRMVVKIGDFGISKILSSKSTPCYISP ELCEGKPYNQKSDIW  
ALGCVLYELASLKRAFEAANLPALVLKIMSGTFAPISDRYSP ELRQLVLSLLSLEPAQRP  
PLSHIMAOPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQ RGIIMTFGSGSNGCLGHGS  
LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEP LLSIDLGTAHSAAVTGEEDL  
GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPD KCCWRHKQCTGHIYPFASDCV  
RHS LHLHSVNHCNCSRLKDSSSEDSSSRGAGPTCSH VIESPCFELTPEEEHVERFRYGW  
CKSYRPVSVAVIHHPLYHECGADDLNXXKRKR RRRRKS KPPIPTQVGPATASPD LGTSMAT  
GTPDSTAPITIWRSSEPTGKGQGSKVIKKVKKKKEKEK DKEEMDEKAKLKKKAKKGQ LTK  
KKSPVKLEPSPPDVSRSL SARQLARMSSESPES REELESSEDSYNGRGQ GELSSEDI VESS  
SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232\_AA836348\_H  
MSVLGEYERHCDSINSDFGSES GCGDSSPGPSASQGP RAGGGAEEQEELHYIPIRVLGR  
GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEI VILALLQHDNI IAYYNHFM D  
NTTLLIELEYCNGGNLYDKILRQKDKLFEEEMVWYLFQI VSAVSCIHKAGILHRDIKTL  
NIFLTKANLIKLDYGLAKKLNSEYSMAETLVGT PYYMSPELCQGVKYNFKSDI WAVGCV  
IFELLTLKRTFDATNPLNLCVKIVQGI RAMEVDSSQYSLELIQM VHSCLDQDPEQRPTAD  
ELLDRPLLKRKRSSSTVTEAPIAVVT SRTSEVYVWGGGKSTP QKLDVIKSGCSARQVCAG  
NTHFAVVTVEKELYTWVNMQGGTKLHGQLGHGDKASYR QPKHVEKLQGAIRQVSCGDDF  
TVCVTDEGQLYAFGSDYYGCMGV DKVAGPEVLEPMQ LNFFLSNPVEQVSCGDNHVVLTR  
NKEVYSWGCGEYGRGLDSEEDYYTPQKVDVPKALI I VAVQCGCDGTFLLTQSGKVLACG  
LNEFNKLGLNQCMGSIINHEAYHEVPYTT SFTLAKQLS FYKIRTIA PGKTHTA AIDERGR  
LLTFGCNKGQLGVGNYKKRLGINLLGGPLGGKQVIRV SCGDEFTIAATDEKVLNSKTIR  
SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQQESET PDPSGGFRGTMEADRGM EGLISP  
TEAMGNSNGASSCPGWL RKELENAEFIPMPD SPSPLSAAFSESEKDTLPYEELQGLKVA  
SEAPLEHKPQVEASVTELF AFESQLVTSAESCSNL CWEGNTDSSCVCVQLSAGG

SEQ ID NO: 233\_R86668\_H, MKK6\_H  
MNLLLSYRDVQDYSAILVELTQLALPTCDVAEQHN VCFHYTFALNRRNRPGDRAKALSV  
LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYH WYRKAFDVEPSLHSGIN  
AAVLLIAAGQHFEDSKELRLIGMKLGCLLARKGCVEKM QYYWDVGFYLG AQIILANDPTQV  
VLA AEQLYKLNAPIWYLVSMETFLLYQHFRPTPEPPGGPPRAHFWLHFLLOSCQPFKT  
ACAQGDQCLVLVLEMNKVLLPAKLEVRGTD PVSTVTL SLLEPETQDIPSSWTFPVASICG  
VSASKRDERCCFLYALPPAQDVQLCFPSVGH CQWFCGLIQAWVTNPDSTAPAEAEAGAGE  
MLEFDYEYTETGERLVLGKGTYG VVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH  
RRLRHKNIVRYLGSASQGGYLKIFMEEVPGGSLSSLLRS VWGPLKDN ESTISFYTRQILQ  
GLGYLHDNHI VHRDIKGD NVLINTFSGLLKISDFGTSKRLAGITPCTETFTGT LQYMAPE  
IIDQGPRGYGAADIWSLGCTVIEMATGRPPFHELGSQAAMFQVGMVKVHPMPSSLSA

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## FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTLGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN  
 STTQSQTFFPCPQAPSQHPPSPPKRCLSYGGTSQLRVPEEPAAEEPASPEESSGLSLLHQE  
 SKRRAMLAHVLEQELPALAENLHQEQKEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ  
 ELRALQGRRLRAQGLGPALLHRPLFAFPDAVKQILRKQIRPHWMFVLDLSLRAVRAALG  
 VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR  
 EILAGKEREYQALVQRALQRLNEEARTYVLAPEPTALSTDQGLVQWLQELNVDSGTIQM  
 LLNHSFTLHTLLTYATRDDLITYTRIRGGMVCRIWRILAQRAGSTPVTSGP

SEQ ID NO: 234\_PAK6\_H

MFGKKKKKIEISGPSNFEHRVHTGFDPPQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT  
 PIQLAPMKTIVRGNKPKCKETSINGLLEDFDNISVTRSNLSRKESPTPDQGASSHGPCHA  
 EENGFITFSQYSSSEDTTADYTTEKYREKSLYGDDLDPPYRGSHAQNGHVMKMKHGEA  
 YYSEVKPLKSDFAFSADYHSHLDSLSKPSEYSDLKWEYQRASSSSPLDYSFQFTPSRTA  
 GTSGCSKESLAYSESEWGPSLDDYDRPKSSYLNQTSPOPTMRQRSRSGSGLQEPMPFG  
 ASAFKTHPQGHSYNSYTYPRLEPTMCIPKVDYDRAQMVLSPLSGSDTYPRGPAKLQPS  
 QSKSGYSSSSHQYPSGYHKATLYHHPSLQSSSYISTASYLSSLSLSSSTYPPPSWGSSS  
 DQQPSRVSHEQFRAALQLVVSPPGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM  
 DLRKQQRRELLFNEVIMRDYHHDNVDMYSSYLVGDELWVMEFLEGGALTDIVTHTRM  
 NEEQIATVCLSVLRALSYLHNQGVHRIKSDSILLTSDGRIKLSDFGFCQVSKEVPKR  
 KSLVGTPYWMAPVISRLPYGTEVDIWSLGIMVIEMIDGEPPYFNEPPLQAMRRIRDSLP  
 PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235\_SURTK106\_H

MNDRNEIQMEAKLQSLTIIAQEILCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI  
 LCGPSREGDSPVAMGMTRMLLECSLSDKLCVIEKQYEVIIIVPTLLVTIFLILLGVILWL  
 FIREQRTQQQSGPQGIAPVPPPRDLSWEAGHGGNVALPLKETSVENFLGATTALAKLO  
 VPREQLSEVLEQICSGSGCPIFRANMNTGDPSKPKSVILKALKEPAGLHEVQDFLGRIQF  
 HQYLKGKHNVLVLEGCCTEKLPLYMVLEDVAQGDLLGLFWTCRRDVMMDGLLYDLTEKQ  
 VYHIGQVLLALEFLQEKHLFHGDVAARNILMQSDLTAKLCGLGLAYEVYTRGAISSTQT  
 IPLKWLAPERLLLRLPASIRADVWSFGILLYEMVTLGAPPYEPVPTSILEHLQRRKIMKR  
 PSSCTHTMYSIMKSCWRWREADRPSRELRLRLEAAIKTADDEAVLQVPELVPELYAAV  
 AGIRVESLFYNYSML

SEQ ID NO: 236\_AA098024\_M

LQEKHLFHGDVAARNILIQSDLTPLKCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL  
 LRPASIRGDIWSFGILLYEMVTLGAPPYEPVPTSILQYLQRRKIMKRPSSCSHAMYNIM  
 KCCWRWSEDSRPLLQVLLQRLLEAASRSADDKAVLQVPELVPELYADVAGIRAESISYSF  
 SVL

SEQ ID NO: 237\_SGK2ALPHA\_H

MNSSPAGTPSPQPSRANGNINLGPSANPNQAQPTDFDFLKVIGKGNYGKVLLAKRSDGAF  
 YAVKVLQKKKILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLVDYVNGGE  
 LFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDGFL  
 CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDQVS  
 QMYENILHQPLQIPGGRTVAACDLLQSLHKKDQRLGSKADFLEIKNHVFFSPINWDDL  
 YHKRLTPFPNPNVTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPE  
 DDDILDC

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## FIGURE 1BB

SEQ ID NO: 238\_CCRK\_H  
MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREIKALQEMED  
NQYVVQLKAVFPHGGGFVLAFAEFMLSDLAEVVRHAQRPLAQAVKSYLQMLLKGVAFCHA  
NNIVHRDLKPANLLISASGQLKIADFGLARVFS PDGSRLYTHQVATRSVGCIMGELLNGS  
PLFPGKNDIEQLCYVLRILGTFNPQVWPELTEL PDYNKISFKEQVMPMLEEVL PDVSPQA  
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPI PQR LGGPAPKAHPGPHIH  
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA  
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS  
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239\_TESK2\_H  
MDRSKRNSIAGFPFPRVERLEEFEGGGGEGNVSQVGRVWPSSYRALISAFSRLTRLDDFT  
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG  
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYS AVVA  
DFGLAEKIPDVSMGSEKLAVVGS PFWM APEVLRDEPYNEKADVFSYGI ILCEI IARIQAD  
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTL EEILSRL  
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLD D K I P H K S P C P R R T I W L S R S Q S D I F S R K P  
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDL MGGKIKFFDLPSKSVISLVFDLDAPGPG  
TMPLADWQEPLAPPIRRWRSLPGSPEFLHQEACPFV GREESLSDGPPPRLSLKYRVKEI  
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEERPAGSTPATF  
STSGIGLQTQ GKQDG

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## FIGURE 2A

SEQ ID NO: 1\_X69117\_H BARK2\_H  
ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCACTTACCTGATGGCCATGGAGAAGAGC  
AAGGCGACCCCGGCCGCCCGCCAGCAAGAGGATCGTCCTGCCGGAGCCCAGTATCCGG  
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT  
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA  
CCTCAGGTGAAGTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC  
CGCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTTTTCTCTGT  
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA  
GTGACATCAACTCTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC  
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCAGTAGATTTTGTGAGTGGAAAAACGTT  
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA  
GGATTCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA  
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA  
ATCATGTTGTCTCTTGTGACGACAGGAGACTGTCTTTCATTGTATGTATGACCTATGCC  
TTCCATACCCAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGGATTTGCAC  
TACCACCTTTTCAACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA  
ATCATTTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTCTACAGAGATTTGAAGCCA  
GCAAATATTCTCTTGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC  
GATTTTTTCCAAAAGAAGCCTCATGCGAGTGTGGCACCCATGGGTACATGGCTCCCGAG  
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG  
CTTTTCAAACCTCTGAGAGGTCACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT  
GAAATTGACCGAATGACACTACCGTGAATGTGGAACCTTCAGACACCTTCTCTCCTGAA  
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC  
GGAGGCGGCTCACAGGAAGTAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT  
GTCTACTTACAAAAGTACCCACCCTTGATTCTCCTCCCGGGGAGAAGTCAATGCTGCT  
GATGCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT  
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTTCATCTCTGAACGCTGGCAGCAAGAA  
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG  
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT  
ATGCACGGGTACATGCTGAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT  
TTTTACCTCTTCCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA  
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAAATGCATT  
TTGTTTCAATAAAAGGAGGGGAAACAATTTGTCTTGAATGTGAGAGTGATCCAGAGTTT  
GTGCAAGTGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCTGT  
GCCCCGAAGTTCCTCAACAAACCTCGGTACAGGTACTGTGGAGCTCCCAAAGCCATCCCTC  
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2\_AA144574\_M BARK2\_M  
CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA  
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCCAAAAGAAGCCTCATGCCAG  
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG  
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC  
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA  
CGTGCACTTCCAGATGCCTTCTCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGTCTCA  
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCACGAGAGTTGAAGGAGCA  
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT  
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA  
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC  
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA  
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

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## FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA  
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTACCTGTTCCCAACAGACTGGAGTG  
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA  
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTAGTCAGGATAAAGGGAGGGAAGCAATT  
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC  
CTTCAATGAGGCCAGAGACTGCTGCGCCGTGCCCCAAATTCCTCAACAAACCACGGGC  
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC  
CACAGAGCAGCGGGGCCTGAAGGAGGGGCCAGCTCTTCAGCCCAGGAGTGGAACGAAG  
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTGAGCACTGACGGGGCTGCTCCA  
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG  
TCCTATCCCACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3\_AA826850\_H

GAAGAGGATGGGCTCGTCCATGTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA  
GGAGGACGTGAACTTCGACCACTTCCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG  
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA  
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCGGGAGCTGGAGATCCT  
GCAGGAGATCGAGCACGTCTTCTGGTGAACCTCTGGTACTCCTTCAGGACGAGGAGGA  
CATGTTTCATGGTCTGAGACCTGCTACTGGGCGGGACCTGCGCTACCACCTGCAGCAGAA  
CGTGCACTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA  
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA  
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA  
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT  
TGTCACGGCGGGGACCGGCTACTCCTTCGAGGTGGAATGGTGGTGGGGGTGATGGC  
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC  
CCTGGTGCAGCTGTTTCAGCACCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT  
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGCTGTGAGTGGGACCACTGAGCGAGAAGAG  
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTCTGCACTGCGACCCCACTTTGAGCT  
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA  
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG  
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTAACAGAGAAAAGCTGAAGAGGAGCCA  
GGACCTCCCGAGGGAGCCTCTCCCCGCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA  
GGACGAGGCGGAACGCTCCGCCCTGCCATGTGCGGCCCATTTGCCCTCGGCCGGGAG  
CGGCTAGGCCGGGATGCCCGTGGTCTCACCCCTGAGCTGCTTTGGAGACTCGGCTGCC  
AGAGGGAGGGCCATGGGCCGAGGCCTGGCAATTCACGCTCGTGGTGGTGCAGGGGACAAGAG  
GCCCCAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG  
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG  
GGACAGGAGTCTTTGTCCCTGCTCAGCCCCGAGGCTGTGCACGGCCCTCGTCACAAGGTG  
ACCCTTGACGACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC  
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAACCTGCTCCAGCA  
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCCTC

SEQ ID NO: 4\_AA960957\_H

GTCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG  
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA  
CTTTGACCATTTTTCAGATTCTCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT  
CGTGCAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG  
CATCGAGAGGGATGAGGTTCCGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

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FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT  
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTCCAC  
AGAGGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG  
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACAACGGACA  
TGTTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC  
CATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG  
CCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT  
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTCAACAT  
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT  
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG  
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG  
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGAT  
TCTAGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA  
TGGCACAAGGACAGCTGCCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG  
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA  
GCTCTTGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG  
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTG  
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGC  
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGGA  
GCTGGGAAGCCTGGGTTCTGGTCCCCTCTCCATGACTGATTACGTGTGACCTCAGACAA  
GTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC  
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT  
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC  
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCAGATCCTAGCTTGTAGA  
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCTT  
CTATGAAAAACAGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT  
CTGGCAGGCCACAGTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC  
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTT  
AGTTTCAGCAGTCTCACCACCACATATCCCCAGTGTGGGATGGCACACAGGTGTCCA  
TTCAGATGAGAGTTGGGTGCGCTGAGCATTGGTTACTCCTGCAGAGTGAATCAGCACCCC  
ATCCAACCTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAACCTCTCTATCAGCTTTC  
AGGGTTTTCTCTCCTGGGAAGGGTGTAATAATCAGCTTGTGAGATTCTTCTTACAGAGAGT  
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG  
AAAGTTTATTTTCAAGGAGGAAAAATGGGTTACACAAAAAGCAAACTACATTCTGATCTGCT  
CAGGGAGAAGCTTGCCTTTGAACTGGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT  
TGGAGTCAGGTTTGTGTTTCAAAATCCAGCCCTGCTGGCTACTAACTAAGTGGGAGACCTT  
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCTATTTTAAACAGGGATAATAAA  
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG  
GATGACTCATAGAAATGGCCTTTTTTGTGACGATAATCGTCATCATTATTTAGATACTTTC  
TTCCTTCACTCACCCAGCAGGTGAGTTTTCTGTGCAAAACAACTGTTTAGGATTCTTCC  
AAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG  
TTTTTATTTTTTTCATCCAACCTCCATTTTTTCACTTTTACATGATTACTCAATCCTTGGG  
GCTGTCCATGTCATCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTAT  
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTTC  
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTGTTTGCACTTTTCTTTACTTCATGTCCC  
CATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGCTGCTCCTCTCCCT  
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCAGGA  
ATTAGGGGAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCCTGGTCTGTTCAAGT  
TGGCATTTCTGTTTGGAAATAAACTATTTCTTGGACATTCTTC

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## FIGURE 2D

SEQ ID NO: 5\_TBK1\_H  
TCCTGAGTCTCGAGGAGGCCGCGGAGCCCCGCCGGCGGTGGCGCGGCGGAGACCCGGCTG  
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC  
TTTTATCTGATAATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA  
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG  
ATGTTCAAATGAGAGAATTGAAAGTGTTGAAAAAACTCAATCACAAAAATATTGTCAAAT  
TATTTGCTATTGAAGAGGAGACAACAAGACATAAAGTACTTATTATGGAATTTTGTCTC  
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCCTTCTAATGCCTATGGACTACCAGAAT  
CTGAATTTCTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG  
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC  
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT  
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC  
TAAGAAAAGATCATCAGAAGAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA  
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA  
ATAAAGAAGTGATGTATAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC  
AGAAAGCAGAAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCAGTCTTT  
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAAACATCCTTGAAGCAGATCAGG  
AAAAGTGTTGGGGTTTTGACCAGTTTTTTGCAGAAACTAGTGATATACTTCACCGAATGG  
TAATTCATGTTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCTCAAAATC  
ATACTGCTACTATATTTTTCATGAACCTGGTATATAAACAACCAAAATTTATTTCTTCAAATC  
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACAT  
TCCCTAAACTACTGAGGAAAACCTATATTTGTAGTAAGCCGGAACCTCTGAATACCA  
TAGGATTAATATGAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG  
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAAATGGCA  
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTA  
TTAAAGATGATTACAATGAACTGTTCAAAAAAGACAGAAGTTGTGATCAATTGGATT  
TCTGTATCAGAAACATTGAAAAAAGTGTGAAAGTATATGAAAGTTGATGAAGATCAACC  
TGGAAAGCGGCAGAGTTAGGTGAAATTTTACAGATACACACCAAAATGTTGAGACTTTCCA  
GTTCTCAGGGAAACAATAGAAACAGTCTTTCAGGATATCGACAGCAGATTATCTCCAGGTG  
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG  
AAAAACTACAAGTCTGTTAAATTGATGACAGAGATTACTATCAGTTCAAAAAAGACA  
AAGCAGAACGTAGATTAGCTTATAATGAAGAAACAAATCCACAAATTTGATAAGCAAAAC  
TGTATTACCATGCCACAAAAGCTATGACGCACTTTACAGATGAATGTGTGTTAAAGATG  
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCACTTTAGGAAACAGT  
TATTATCGCTGACTAATCAGTGTGTTGATATTGAAGAAGAAGTATCAAAATATCAAGAA  
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAATGTTTACAGCTTCCAGTGGAAATCA  
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA  
TGAAGAAATTAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAAAACCACA  
TTTGTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTGACTGTCTTT  
AGCTTTCTAATAGAAGTTTAAAGAAAGTTTCCGTTTGCACAAGAAAAAACCCTTGGGCA  
TTAAATGAATGCCTTTATAGATAGTCACTTGTCTTCTACAATCCAGTATTTGATGTGGTCG  
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTGGCTGCTGTGAA  
GATGTAATTTTATCTTTTAACTTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC  
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTTACTCTGAGTGGGGC  
TAAATAAGTTATTTTCTCTGACCGCTACTGGAAATATTTTAAAGTGAACCAAAATAGG  
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAAATGGTAGAACGGTGGCTAC  
TGTGAGTGGGGAGCAGAACCGCACCCTGTTATACTGGGATAACAATTTTTTGAAGG  
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCAGATCCAGTTATCCTTGTATCCATG  
TAATTTTCAGATGAATTATTAAGCAACATTTTAAAGTGAATTCATTATTAATAAACTATT  
ATTTTTTCTTTTGGCCATAAATGTGTAATTGTCAATTAATTTCTAAGGTCAATTTCACT

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## FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT  
CAATTTTAAAAAA

SEQ ID NO: 6\_AA305176\_H

TGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCGCTGTAGGCTGTCCAGCGATGGATCC  
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG  
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATTAGCCG  
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTTGTATGCAGTAAAGGT  
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA  
TGCACTGGCACTAAGCAAAAGCCCATTCATTGTCCATTTGTATTATTCACTGCAGTCTGC  
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCTACA  
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC  
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT  
TATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA  
TAGAGATATTAATATGATGGATATCCTTCAACACCATCAATGGCAAAACCTAGACAAGA  
TTATTCAAGAACCCAGGACAAGTGTATCGCTTATCAGCTCGTTGGGATTTAACACACC  
AATTGCAGAAAAAATCAAGACCTGCAACATCCTTTCAGCCTGTCTGTCTGAAACATC  
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGACACTACGCCTTA  
TTCTAGCAAATTAATAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT  
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG  
TAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG  
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA  
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCCATAAAGAAATGAAATTGTGA  
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCTGACATTCTGTCAAATTC  
TTTTGAAATATTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA  
GATTCTTGCAATAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT  
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTGTTTTGTTTTATTTTGT  
TTTTAACATATGTCAATTTAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7\_AA116841\_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG  
CAATGGACATGCTTTTAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC  
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTCCG  
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC  
ATCTGACCGTATCTGGGTTAGTCTGTAGCACATGCGTGTCAATTTTATCTAACTTGTGA  
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA  
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG  
AATTAATAACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA  
GCCATAATAGCTTTTTTTCATCTTATTCTACTGCACTTTATGAAGAGCAAAGTATCAA  
TAACTAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8\_AA256100\_H

AGGGAGCTGACGGGCGCCCGGCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCCGCGGGC  
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC  
TATGAGCAACCATACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTA  
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC  
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAGAAAAGTTACGTGATCACAAACAGCTCG  
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC  
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC  
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAAGAGCAGGT

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## FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA  
GATGTTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG  
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT  
CTACATTTTCAGAGACTGTTCTGGCAATAGATGGGATCCACCAGTTGGGTTTTCATCCATCG  
GGATATTAAGCCAGACAACCTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT  
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTATAGAAATCTCACACA  
CAACCCACCAAGTGACTTCTCATTTCAGAACATGAACTCAAAGAGGAAAGCAGAACTTG  
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC  
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT  
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA  
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA  
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG  
TGGAGTAGAAGAAATAAAGGTCTCCCTTTTGAAGGTGTGCGACTGGGAGCACATAAG  
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA  
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACCGGACTACAA  
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG  
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA  
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC  
TGAAATACTCCTGAAGATGGTGGTGCTTATTGACTACAAGAGGAAATCTACAGGATTAG  
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTAAATAT  
TTTATTATTTTTGTAACTTTATTATATGAAGGTACTGGAATAAAAGGAACAGACATCCC  
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT  
TTGAACTGTAAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG  
CTAACCTGTAGGTAACTGCAGTATTGATGTTTTACTGCAAATCTTATGGGTCTAGATA  
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTGTAACATTGCCCTATTGGTTTGGACATC  
TGTAAGATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA  
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG  
TGACAAGTTTTATAAAGGAAGACAAAGTTTTAACACCTTCACTCAAGCACTCCACTAATA  
TATTTACGTTGCATTTCAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG  
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAATTTCTT  
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA  
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTATTAACTATTTTTTTAAATGTC  
AAACTTCTATCATGTAAATGGACTTATAGAGAACAAAAGCTATTTACTTTGGTTTTCTA  
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTATTCTTTTGTATGAAAATTTTCTCTT  
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAGATCTT  
GAACAGAGTGGATGTTCACACTGAGTAGAATTTTCTTCTGCTGGGCATGCTGTATTCT  
AGACCTGACAGATCTTTGATAGAGGTGAGTTTAAAGGGCAATATTGTTCTTGTGTTAG  
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTGT  
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATTTCTTGGGTATCTCTCTAAGAATT  
AAATAATCTTTTCTAGCTTAATATTTTAAATCTAATTCAAACAACCTCTGAGGTTTTGGTT  
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAAATGGCCTAATGTTTGTACATAAC  
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA  
TCAAATCTAAAGTGATGAATTTTGTAGGAATGTCTTCTAATGGGGAAGAATTGCAT  
AGGAGCATTATGCAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG  
TGTTTTATAAGGCCATCCTGTTCCCCCAACTCCCCCATTTTGGTTTTGTTCTTTTTAA  
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACTTCCATTTTCTAGTCTGGAT  
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA  
CTCTAATTTTTCTAATTATACTGCCTTTAATTAACATAATATTAATTTGCTGAGGTT  
TATGAGATTTTCTACCCACATCGCTCCCCTTTTTTAAAAAGGACTGTTTTGCTAGTG  
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCTAGTCTAGTATGGTAA

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FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA  
GAAACTGATTTACCTAAGTTTACTTTTAAATTGCATAATAGAGCATTTTTTGTGTTGAGT  
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTACTTTCTTGGCACTGGAAG  
GGTAGTTCTGGAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA  
TTCACAACTCTTGGGGTTTTCTCCTCATCAAAGCATTCTTAAGTGCCTATCTAAAAGC  
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTTCATGATGCAAATTAAGT  
AGATAATTTGCAAAGTACCTTGAGATTGAATTTTCTCTATTATATATTCCCATATTTTC  
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT  
TTCTTTAAATTAGACTCTATTTTGAATTAAGAGTTTATTATAAACCGTGTGTTTTTG  
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTCTGATTTAATG  
TAGACTTTGACTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTCTTT  
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT  
GAAAATAAGGAATTGCTTATAAACAGCCACTTCTGAATACAATATGTAGCTGATTTAAT  
AAGCTAGTTAGTGAATGGAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG  
GCCTAAGATAGGGTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT  
TTTATGTAAATCTCTAAATTTAAATATTTTAAAGTACATTTATTTTGGTGTGTTTTATTGT  
ATAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT  
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA  
ACACATTCTCCTTTGAATTGTTAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC  
CCATGATTATTTTCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCATTAT  
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGGA  
CTACTAGAGATATTTTAGATTTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA  
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTAGCAAT  
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA  
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT  
TAC

SEQ ID NO: 9\_AA210825\_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCACCCCGCTCCGGCAA  
CGCCCCCTTCCCTACGGCTCCCGACCGAATTTTCTCCAATTTCTGCGACTCGTGAGATT  
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCCTGGCCGGTCCGGTCCC  
TGCGAACCCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA  
CCCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCTGCCAGATCTTTTCTCGGATCCC  
CGCTCTCCACCACCTGCTCAGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGGC  
CCCCCGGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCCTCCCCCATGGCCAC  
CGCCCCCTCATTATCCCGCCGGGCTCCCTGGCTCTCCCGGGCCGGGGTCTCCTCCGCCCC  
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCGGGTT  
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCGTGCTGTTGCCCGCCG  
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGACAGAGTTCCTTG  
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCGG  
CCAACCTCCTGCAGCTGGTGCCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG  
TGGTGTGCTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG  
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG  
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAATACCACAAGCGCTGTGCCTTCA  
GCATCCCCAACAATGTAGTGGGGCCCGCAAACGGCGCCTGTCTACCGTCTCTGGCCA  
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA  
GCCGTAGCACACCGAACTCCTGCCTCGCCGTCCCCGTCTCCTCTTCTCTCTCTG  
CCTCATCGTATACGGGCCGCCCATTTAGACTGGACAAGATGCTGCTCTCAAGGTCAAGG  
TGCCGCACACCTTCTCATCCACAGCTATACGGGCCACCGTTTGCCAGGCTTGCAAGA  
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC



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## FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG  
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG  
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG  
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA  
GGGTGGTGCAATCGGTGCGACACACGACGCGGAAATCCAGCACCACGCTGCGGGAGGGT  
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCTGGAGT  
GCAAGTGTATCAGCTCTTCCAGAACAACGACCAACAGATACTATAAGGAAATTCGCG  
TGTCAGAAATCCTCACGGTGGAGTCCGCCCAGAACTTCAGCCTTGTGCGCGCCGGGCACCA  
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG  
GCGGGACTCCGGGTGGGCAAGTGGGCAGGGGGCTGAGGCGCGCCGGGGCTGGNNGAGA  
CAGCCATCCGCCAGGCCCTGATGCCCGTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC  
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA  
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT  
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGAGCTCCGGAATGAAGTGGCATA  
TTGACAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCATTTC  
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCCTGAGA  
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG  
AGAAGGGCCGGCTGCCTGAGCGCTCACCAAGTTCCTCATCACCAGATCCTGGTGGCTT  
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC  
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA  
TCGGCGAGAAAGTCGTTCCGCGCGCTCAGTGGTGGGCACGCGGCCTACCTGGCACCCGAGG  
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT  
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC  
AGAACGCGCGCTTCATGTACCCGGCCAGCCCTGGAGCCACATCTCAGCTGGAGCCATTG  
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC  
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA  
AGATGGGAGAGCGATACATCAGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG  
CAGAGCATCCGCTGCCTGGGTCTGGGCTGCCACGGACAGGGATCTCGGTGGGGCCTGTC  
CACCACAGGACCACGATGACAGGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCTCTG  
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTACAGGATCCAGCAATGAACTG  
TTCTAGGGAAAGTGGCTTCCCTGCCCAAAGTGGATGGGACACGTGGGGAGTGGGGTGGGG  
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCAGCAATTAAACGGACTCATCTCTGGCC  
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10\_AA127299\_H  
ATTCAATTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT  
GATCCTTACATCAAAATCACAATCTTTCTCAAAAAACGAAAGTGATTAAGAAAACTTTG  
ACTCCAATTGGAATGAACTTTTTTGTGCATTTTCCAGAAAAACAACCTTGAATTA  
GAATGTTGGGACACGATACTTTTTTTCAGATGATTTTATGGCAAGGCTTCCATTTCTTG  
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAGGA  
GAATTTGCAGGAAAA

SEQ ID NO: 11\_AA316804\_H  
ATGTCTGCAAATAATTCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCCT  
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCTTAAGACGGGACTCTCTGCCCGACTC  
TCTAATGGAAGCTTCAGTGACCATCACTACCAACTCCAGAGGCTCAGTGACATACAGTT  
TCATTTCTACTGCAAATTGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG  
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT  
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTCGCCATGACATGAAGTCCAGAAAAC  
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

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FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTTCGTCCACATACTCTCTATGTACAT  
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT  
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT  
CCAAATAACTGTAGTGGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC  
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCAGTGAAGAGTCA  
CATGTCCACCAGGAACCAAGTAAGAGAATTCTCTTGGAGTGGTCGCCCAATCTGGATG  
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC  
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG  
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC  
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCCTTCCAGTCTGGGAACAGATACAGATATA  
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA  
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG  
GAAAGAGATGAAGAAGCCGTTAAAACAATCAGTCCATCAACAAGCAATAATATTCGCTA  
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA  
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT  
GACAGCAAAATGTCTAACATTATTTCAGAATGAATCTGGATCAAAGTATTATAAGGAAAT  
CCACTTTCAGAAATCTCCGCATATCTTACCACGAGATTTCAAAACATTTACAAGGC  
AGCAATCCACACTGTTTTGAAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC  
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA  
CAGAGCTGGGAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT  
TGCACTTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT  
AATTGTGAGATTGAGGAGATGTGGATATCAGTACTGTTTACCAGATCTTTCAGATGAG  
GTGCTTGGTTTCAAGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG  
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC  
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT  
ATGTTTGAAACCCCAAGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG  
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC  
ACACAGATACTTGTGCTTTGAGGAATCTGCATTTTAAGAATATGTGCACTGTGATTTA  
AAGCCAGAAAATGTGCTGCTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC  
TTTGGATTTGCACGCATCATTGGTGAAAAGTCATTTCAGGAGATCTGTGGTAGGAACCTCA  
GCATACTTAGCCCTGAAGTCTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG  
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAATGAGGATGAA  
GATATAAATGACCAAATCCAAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA  
ATTTCTGGTGAAGCAATTGATCTGATAAACAATCTGCTTCAAGTGAAGATGAGAAAACGT  
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC  
CTTAGAGAATTTGAAACTCGCATTGGAGAACGTTACATTACACATGAAAGTGATGATGCT  
CGCTGGGAAATACATGCATACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT  
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12\_PKNBETA\_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG  
GAGGTGATCCGCGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG  
CGGCGCGTGGCCACAGACCGCGGCCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCTCTC  
AACC GCGCCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG  
CCCCGCGCTGGGCTGGCCAGCTGAGCCTGTGGCCTCAGGACCCCGCGCTGGGCGAG  
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG  
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCAAGGAGAGGAAG  
CTCCTTGCAGCTGCCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG  
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGAGCCAGGGCCTGAGCTACTGGCG  
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGCGCCAAGAAGCTG

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## FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGCC  
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG  
GAGCAACTGCCTCCTGCCACCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG  
GTGCCTGGATAACCCCGAGCCTTCAGGGACACCTGTGAAGCCACCGCCCTAACAGGGACA  
CTGCAGGTCCGCCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA  
GCGGCCGCACTGGCCAGCAGCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG  
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGT  
GTGGGGCAGACGGGCTGGGGGAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTCATC  
CCACTGGAGCGAGCCCTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA  
TGTGGCGTGGCCTTCTGAGACTTGAAGACTTCCTGGACAATGCCTGTACCAACTGTCC  
CTCAGCCTGGTACCGCAGGACTGCTTTTGGCCAGGTGACCTTCTGCGATCCTGTCAAT  
GAGAGGCGGCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGAGAGGCCAGGAC  
TTCCTGAGGCGTTTCGCAGATGAACCTCGGCATGGCGGCTGGGGGCGCCTCGTCATGAAC  
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC  
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCAGTAATTTCTGCCCAAGAAG  
ACCCCTTGGGTGAAGAGATGACACCCCCACCAAGCCCCACGCCTCTACCTCCCCAG  
GAGCCAACATCCGAGGAGACTCCGCGCACCAACAGTCCCCATATGGAGCCTAGGACTCGA  
CGTGGGCCATCTCCACCAGCCTCCCCACAGGAAACCCCTCGGCTTCAGGACTTCGCG  
TGCTTAGCTGTGCTGGGCCGGGACACTTTGGGAAGGTCTCCTGGTCCAGTTCAAGGGG  
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGACGAG  
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCT  
TTCTGTCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCGCTTTGTGACTGAG  
TTTGTGCTGCTGGTGGTGAACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG  
GCCCCCTTACGTGGCTTGTGTTGCTCCTGGGCTGCAGTTCTTACACGAGAAGAAGATC  
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCAGGGATTCTGAAGATC  
GCAGACTTTGGACTCTGCAAGGAAGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT  
GGCACCCCGAGTTCCTGGCTCCCCGAGGTGCTGACCCAGGAGGCATACACAGGCCGTC  
GACTGGTGGGCGCTGGGTGTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA  
GGGGACACAGAGGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCGGC  
TTTCTGTGCGTGCAAGGGCTTGAGTTCATTGAGAGCTCCTCCAGAAGTGCCCGGAGAAG  
CGCCTCGGGGAGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC  
ACCAACTGGCAAGCCCTGCTCGCCCGACCATCCAGCCCCCTTCGTGCCTACCCTGTGT  
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACC  
CCACCTGCACCCACAGCCTCCTCACTGCCCGCCAACAGGCCGCTTCGGGACTTCGAC  
TTTGTGTGAGAGCGATTCTGGAACCTGA

SEQ ID NO: 13\_AI021023\_M PKNBETA\_M  
GCTGAAGTGGGATAACCTTCTGCTGGATGCCAGGGATTCTGAAGATCGCAGACTTTGG  
ACTCTGCAAGGAAGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA  
GTTCTGGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGGCTGTGGACTGGTGGG  
GCTGGGTGTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA  
GGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCGGCTTTCTGTGCGT  
GCAAGGGCTTGAGTTCATTGAGAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGG  
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA  
AGCCCTGCTCGCCCGACCATCCAGCCCCCTTTGTGCTACCTGTGTGGCCCTGCGGA  
CCTGCGCTACTTTGAGGGCGAGTTACAGGGCTGCCGCTGCCCTGACCCACCTGCACC  
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCTTCGGGACTTCGACTTTGTGTGAG  
GCGATTCTGGAACCTGAGGGCATCTCCTGGCACCTCTGTCCCCTTCCCCACAGACTG  
TTAGAGCCTCTGCTCGTTACCCGTCGCGCTGCTGGAGGTCCAGGCCTTGCTGGGTAC  
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGCTCAG

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## FIGURE 2K

TGTCACTGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA  
GACCTGGCCCAGAAAGGGTGCCGAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG  
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14\_H19102\_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA  
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAACCTACGGGGGCACCACTATCTGCACCAG  
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGGCCAGTGCCT  
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG  
CTGAAGATTTTAGGCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTCAAGGTGCTAGAT  
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCAAGGTAAAGTCCCTACAGAGG  
GATACCGTGAGGCAGTGCAAAGAGGAGGTAGCATCCAGCGACAGATCAACCATCCCTTT  
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC  
TGCAGCACAGATCTGTACTCCCTTTGGTCTGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC  
CGTCTCTTTGCTGCCGAGTTGGTGTCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG  
CATCGAGATGTGAAGATGGAGAATATTCTTAGATGAACGAGGCCATCTGAACTGACA  
GACTTTGGTCTGTCCCGCCAGCTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT  
CTTCAGTACATGGCCCCAGAGTCTTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG  
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGCGACTGGAAAGTTTCCAGTGGCTGCAGAG  
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCCAGCTTCT  
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCTCCATCGT  
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTGCGGGTGTGGCCTTCGACCCA  
GAGCTCCTACAGAAGCAGCCAGTGAAGTTTGTACGGAGACACAAGCTACCCAGCCAGT  
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC  
CCTATCCCTGCTTGA

SEQ ID NO: 15\_AA476563\_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAACTCCTGGGACTTGACTTT  
GGAGAAAAATGTATAGTCTAAAATCAGAACCTTTGAAACCATTCTTTACTCTTCCAGAT  
GGAGACAGTGCTTCTAGGAGTTTTAATACTAGTGAAGCAAGGTAGAGTTTAAAGCTCAG  
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT  
TTTGATGATGTCACTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT  
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT  
ATAGGGATAATAGAAAATAAACTCTTGGAAGCCCTGATGTTTATGCCTCAGGCTTAGT  
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAAGTGAAGTATCCCTCTGGG  
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT  
GTAGCAGCTGTTGATCATAGTAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT  
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAAGTGAACCAACACAGAAGAAAGC  
TTATTCCTGATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT  
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA  
CCAATTCTTTATTCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA  
GGAGACAAGGAAATACATCAGATTTTGGAGACCTTGATAAAAAATTAGCACTAGCCTCC  
AGGTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT  
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTGTAACCCAAACAACATCTTATTG  
AATGATAGAGGACACATTACGTAACGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC  
TGTGACAGCGATGCCATAGAGAGAAATGTACTGTGCCCCAGAGGTTGGAGCAATCACTGAA  
GAACTGAAGCCTGTGATTGGTGGAGTTGGGTGCTGTCTCTTTGAACCTCTCACTGGC  
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA  
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAAGTCAATCCTCTG

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## FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGAAGATATCAAATCTCATCCATTTTACC  
CCTGTGGATTGGGCAGAACTGATGAGATGA

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ATGCTACCATTGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTACGCGG  
GGCGGCGGAGCAGCGGCGAGGTAAATGGTCTTAAATGGTTGATGAGCCAATGGAAGAG  
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTTAAAGAAATCCCTATTACTCATCAT  
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGTT  
CAGGGGTCATTTGGAAAGGTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG  
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTAAAGTTTCGAGACAGAGTTCGGACA  
AAGATGGAGAGGGATATACTGGTGGAGTAAATCATCCATTTATTGTCAAATTGCACTAT  
GCCTTTCAGACTGAAGGGAAGCTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT  
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA  
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG  
CCAGAAAACATTTTGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC  
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG  
GCTCCTGAAGTAGTAAATAGGAGAGGCCATTCCCAGAGTGCTGATTGGTGGTCATATGGT  
GTTCTTATGTTTGAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG  
ACCATGAATATGATATTAAAGCAAACTTGGAAATGCCTCAATTTCTTAGTGCTGAAGCA  
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA  
GTTGAAGAAATCAAAGACATCTGTTTTTGGCAAATATTGACTGGGATAAATTATATAAA  
AGAGAAGTTCAACCTCCTTCAAACCTGCTTCTGGAAAACAGATGATACTTTTGTGTTT  
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAT  
GCTCATCAGCTCTTCAAAGGATTGAGCTTTGTTGCAACTTCTATTGCAGAAGATATAAA  
ATCACTCCTATCACAAGTGCAATGTATTACCAATTGTTGAGATAAATGGAATGCTGCA  
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGGCTCCTACTCTGTTGCA  
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT  
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT  
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG  
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAATGTTTCTCGGAACGGGAGGCT  
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT  
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGCAAGTTCA  
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACTTCGAGGAGAAAATGGACTTCTCTTA  
ACTCCATGCTACACTGCAAACTTTGTTGCACTGAGGTTCTTATGCAACAGGGATATGAT  
GCTGCTTGATATCTGGAGTTTAGGAGTCCTTTTACACAATGTTGGCTGGCTACACT  
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA  
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTAGACGGAGCAAAGGATTGCTT  
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAGCAC  
TCATGGATAACTCAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA  
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTCAA  
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGAGCATGAAAAGCGA  
ACATCAACTGGCCTGTAA

SEQ ID NO: 17\_AA215680\_H  
ATGAGCCTGGTGGCCTGTGAGTGCCTGCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA  
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTTCGCAACAGGGTGGCTCTGGGA  
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC  
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCCTTCAACCACTATCAGAATGGCGTG  
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAGGAGCGAGTGAGGCTGTGAAG  
CTGAAAATTACCAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

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## FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGGCCATT  
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTCATCGAG  
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC  
AGGTGCCACATGGTGAGCAGGGAGCGGCTGACCATCATCCCACACGAGTCCCCTACATG  
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCTGACACCTGGAGCATGTG  
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCAGGCGCACTCCCGACATTCTGGGCTC  
AGCTCTGGCTCTACCCAGGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG  
ACCCAGCGAGGCTTCCCTCAGGCCATGCCCTGGCCAGGACAGAATCGCCCTGGAGCCT  
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACAGACCCAGAGG  
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGCACCTCTGGCTCCTCGGACCTTCCAAAG  
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAACTCAGACGCTGGG  
CCCCCTCGGGGGCTCACTTGGGTTCTGAGGGGGCGGCCCGGTGCTAGGGGGCTGTGGC  
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGCTGTGGCAGGGCC  
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG  
GAGGCGCTGCACGAGCAGGGGTGCTGTGCCGGGACCTCCACCCGGGAACCTGCTCCTG  
GACCAGGCAGGTACATCCGGCTCACATATTTTGGCCAGTGGTCAGAGGTGGAGCCCCAG  
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG  
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA  
ATGGCACTGTCCCAGAGCCACCTTACAGGAATCCAGGCCCCACCCAGCTCCAGCTGCCC  
GAGTGGCTCAGTCGCCCAGCGGCTCTCTGCTGACTGAGCTGCTGCAGTTTCGAGCCTACC  
CGGCGCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCACT  
ACCATCCAATGGAGCAAGCTGGTGGGTAA

SEQ ID NO: 18\_SGK\_H  
ATGACGGTGAAAACTGAGGCTGCTAAGGGCACCTCACTTACTCCAGGATGAGGGGCATG  
GTGGCAATTCTCATCGCTTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTCAG  
AAGATTGCCAATAACTCCTATGCATGCAACACCCTGAAGTTCAGTCCATCTTGAAGATC  
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCTTCTCCTCCACCAAGTCTTCT  
CAGCAAATCAACCTTGGCCCGTCGTCCAATCCTCATGTAAACCATCTGACTTTCACTTC  
TTGAAAGTGATCGGAAAGGGCAGTTTTTGGAAAGGTTCTTCTAGCAAGACACAAGGAGGAG  
GAAGTGTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAAGAAAGAGGAG  
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCTTTCTGCTG  
GGCCTTCACTTCTCTTCCAGACTGCTGACAAATTGTACTTTGTCTTAGACTACATTAAT  
TCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT  
AGAGACTTAAACAGAGAATATTTTGCTAGATTACAGGGACACATTGTCTTACTGAT  
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACACATCCACCTTCTGTGGCAG  
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTG  
TGGTGCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCTTTTATAGCCGA  
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT  
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAAGGACAGGACAAAGCGGCTC  
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCACTGCTTCTTCTTAATTAAGTGG  
GATGATCTCATTAAATAAGAAGATTACTCCCCCTTTTAAACCAAATGTGAGTGGGCCCCAAC  
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG  
TCCCCTGACAGCGTCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC  
TTTTCTATGCGCCTCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19\_AA107515\_M  
CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCCTCAGTCTCTTTTGGGCTCTTTC  
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCTTACCTACTCCA

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FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA  
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAAACACGCTGAAGTTCAGT  
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC  
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCCCTCCAACCCTCACGCCAAACCCT  
CCGACTTTCACCTTCTTGAAAGTGATCGGAAAGGGCAGTTTTTGAAAGGTTCTTCTGGCTA  
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA  
AGAAGAAAGAGGAGAAGCATATTATGTCAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC  
ACCCTTTCCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC  
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGG  
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC  
TAAACATCGTTTATAGAGACTTAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA  
TCGTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT  
TCTGTGGCAGCCTGAGTATCTGGCTCCTGAGGTCCCTCCATAAGCAGCCGTATGACCGGA  
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT  
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA  
AACCAAATATTACAAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA  
CCAAGAGGCTGGGTGCCAAGGATGACTTTATGGAGATTAAGAGTCATATTTTCTTCTCTT  
TAATTAAGTGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAAACCAAATGTGA  
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT  
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACGGCCAGTGTGAAGGAAGCAGCAGAAG  
CCTTCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCTCTGAGTGCTCCCGGGAT  
GGTCTGAAGGACTTCTCAGCGTTTCTTAAAGTGTCTTTCGTTAGCCTTTGGTGGAGTTG  
CCAGCTGACAGAACATTTTAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC  
CCGGCGTGGCGCGACGCAGCGCGCTGCTTGATGGGAGCTTTCGAAGAGCACACCCCTC  
CTCTCAATGAGCTTGTGAGGTCTTCTTTCTTCTTCTTCTTCCAACGTGGTGCTAGCTCC  
AGGCGAGCGAGCGTGAGAGTGCCGCCTGAGACAGACACCTGGTCTCAGTTAGAAGGAAG  
ATGCAGGTCTAAGAGGAATCCCCGAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA  
ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTCTTATCGCAGAGTGTTCAAGT  
TTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTCCCTTGGCGGATTTCCCGTGTGTGCA  
GTGGCGTGAGTGTGCTATGCCTGATCACAGACGGTTTTGTTGTGAGCATCAATGTGACAC  
TTGCAGGACACTACAATGTGGGACATTGTTTGTGTTCTTCCACATTTGGAAGATAAATTTA  
TGTGTAGACTGTTTTGTAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA  
TGACGAGCATTGAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTAGAA  
AGGGTTTTTATGACCAATGCCCCAGTTGTGAGTCAAAGCCGTTGGTGTGTTTCTATTGTTT  
AAAATGTCACTATAAAACGGGCATTATTTATGTTTTTTTCCCTTTGTTTCTATTCTTT  
TGCATTCCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTTATAACACT  
AGATATTTAAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT  
GGGTATAATATGTACAATTCCTCCTCCTTACCACACAACCTTTTTTGTGTGCGATAAAC  
CAATTTTGGTTTGCAATAAAATCTTGAAACT

SEQ ID NO: 20\_AA109508\_M  
CCACCTGCAGCGGGAGCGCCGGTTCCTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT  
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA  
GAACATTCTCTTGGACTGCCAGGGACACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGA  
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC  
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGTGCTTGGGGGCAGT  
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCCAGATGTA  
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGACAGTGGCCGCTGTGA  
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTT  
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

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## FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTTTTGA  
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC  
CAGCAGCTCTGGGGCCTCAAGTGCATTCTCTGGGATTTTCTTATGCGCCAGAGGATGATGA  
CATCTTGGATTGCTAGAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA  
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAATAACAATGGCTTCAACGAGAAG  
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG  
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT  
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTAG  
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCA  
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG  
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGTTC  
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG  
CCTCCTGGTGTGTTGATTTTGATCTCAATGTGTAAAATGACAGAGATGTAACAAGCTCAT  
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21\_AA887783\_H  
CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT  
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCAGCTCCGATGAACACAGAGAGAAAAAGA  
AGAGGTTTACTGTTTATAAAGTTCTGGTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA  
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCTGCTANGG  
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAC  
AAAGACGAGCAGGACTAAACGAATTCATTGAGACCTAGTTAGGTATCCAGAACTTTATA  
ACCATCCAGATGTGAGAGCATTCTTCAAATGGACAGTCCAAAACACCAAGTCAGATCCAT  
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCAGAACATCAACC  
TGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGATTTCTTAAAGTTATTG  
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAAACGGAACTGGATGGAAAATTTATG  
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAGAGCAAAAACATATTATGG  
CCTTCCAAACAAGCTTAAAGCTTTATTTGTTCTGGAATTTGTTAATGGAGGGGAGGGAC  
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA  
CCACATTTTGTGGGACACCAGAGTATCTTGACCTGAAGTAATTAGAAAACAGCCCTATG  
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC  
CTCCTTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA  
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAACTCCTAGAAAAAG  
ACAGGCCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAATCATCCTTTT  
TTGAATCACTCAGCTGGGCTGACCTTGTAACAAAAGAAAGATTCCACCACCATTTAATCCTA  
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC  
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG  
ATGATGCATTGCTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTGTGAGCAG  
TTTGCCATTGAGAAACCATTTGAGCAAAATAAGTCTATAGATGGGACTGAACTTCTATTT  
GTGTGAATATATTCAAATATGTATAACTAGTGCCTCATTTTATATGTAATGATGAAAAC  
TATGAAAAATGTATTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT  
TGATTAATAATTATATTCTTGTGTTAATAAGCTTATTTTAAACAATTTAAAGCTATTAT  
TCTTAGCATTAACCTATTTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA  
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTAAACAGTCAATTCAGTTCAGCT  
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTATCACACCAAACTAT  
GCAATTGGTACATGGTTGTTAAGAAGAAACCGTATTTTCCATGATAAATCACTGTTTG  
AAATATTTGGTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG  
TTAACAATTGGAATAACTTTATCTGCAGATCATTTAAGAAGTAACAGGCCGGCGCGGT  
GGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCTGAGGCCGGCAGATCACCTGAGGTCA

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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT  
 TGGCAGGGTGTGGTGGCACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA  
 ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG  
 CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22\_R47805\_H

ATGGCGCACCAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA  
 CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT  
 GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGCTGCTGCCACTG  
 CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC  
 TTCGAATGGCTCTTCTCGCCTGGTGCCTGATAACTCCCCCGTGCGGCTGAAGATGCTG  
 TACGCGGCCACGCGGGCCACAGTGAAGGAGGTTTGGAGGTGGCCACATCAAGGATGAG  
 CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGGCTGGGTACCAGAAACACCTGTCGTCC  
 TGTGCGGCACCTGCCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC  
 GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC  
 CCCCTGCAGCCTGAGGCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC  
 ATCCAGATGAAGCTGGACCTAGAGCGGGAACCATAGAGCTGGTGCACACAGAGCCACG  
 GATGTGGCCAGCTGCCCTCCCGGGTGCCTCGAGATGCTGCCCGCTACCACTTCTTCTC  
 TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTCATCTACTCCATGCCG  
 GGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCTCCTC  
 GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG  
 GCAGAGCTGACGGCAGAGTTCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG  
 CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGGCAAGCGGGGCCATAAGCGCCTCATCCG  
 GGCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23\_H60215\_H

CCACGCGTCCGGCGCCCGCAGCCATGGAGGGAGGCGGCGGGCGGGCGGGCTCGGG  
 TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCCGGCCCCCG  
 CGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA  
 CCACCCGGCGAAGTGACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC  
 ACAATATATGTGCTCTGCTCTCTCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG  
 CACCAGGTCTGAATTCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT  
 GACCACAGACCCATTGAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA  
 TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCCGCCA  
 GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAAATAATGCAAAGAGAGCTGGACCATTC  
 TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAGTGCAAGTGTGGCGAGGA  
 AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC  
 AAGGCATAGAGAGCCAGGAAGAGCGGCAAGATGCTGCTGCACACCGAGTACTCAC  
 TGCTGTCTCTCTGCAACGCAGGATGGCGTGGTGCAACCACCGCCTCTTCCAGGACC  
 GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC  
 GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC  
 TCATCAACCTGCAGCACTACGTATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG  
 TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAATATCGTGCACA  
 GAGACCTGAAGCTGGGGAACATGGTGTCTCAACAAGAGGACACATCGGATAACCATCAGCA  
 ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGACCTGCTGAAGGACCAGAGAGGGA  
 GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCGCGGTACCGTGGCAAGCCAGTG  
 ACATGTGGGCCCTGGGCGTGGTGTCTTCCACATGCTGTATGGCCAGTTCCCCTTCTACG  
 ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG  
 ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGACCCCC  
 AGCAGCGCCTGGCCGCCGCCGACGTCTGGAGGCCCTCAGTGCCATCATTGCATCATGGC

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## FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA  
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCAGTACGAGTTTG  
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC  
GGAGCTGGGTACCCAAGCGGCAGTTCCGGCAGCGCACCAACCGGTGCGACGGCTGGGCCACG  
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT  
AACAGCCTCAGCCGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG  
TGGCTGTGAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC  
AGGGACAGGGACAGCCAGGTACACGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT  
TGGGATGATTGCTCGATTGTTTGGTTTTTAATCTGAGAAGCCTAGATAACTAATCTGCT  
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC  
AAGAGGGAGGAGGGAGCCTGCTCACCCTACTCCAGGGCCTTCCCCAGCGGCCACCAACTG  
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGCAGCTCGCTGCAGGCCCC  
AGAGCGAGCTTCCCTCCTCCCTGCTCTCCAGGGCCCTGCCACAGCCTCTTTCCGTCCC  
TCTCTTTCTGATCCAGGCCCTCAGTCCAAGCTTTGGAAAACCTTCACCTCATCTTAAAC  
CAAACCTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24\_SGK324\_H  
GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAG  
CCGCGGCCGGGGTCCGCGAGAGGGGCCCCAGCTCCTCCGGGGGCAGCAGCTCGGGC  
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC  
ACGCGGAACCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG  
AACGGGGACCGCTACTTCAAGGGCCTGGTGTGTTGCCATCTCCAGCGACCGCTTCCGGTCC  
TTCGATGCGCTCCTCATAGAGCTCACCCTGCTCCCTGTGCGACAACGTGAACCTGCCCCAG  
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTACCAGCCTGGACGAGCTG  
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC  
AAAAATATTAATCCAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT  
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAAGAAAGTAAAGATTTTCATCAACCCCAAGTTA  
GTGACTGTGATTGGAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA  
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC  
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG  
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATGTCATGTGGACCAGAAAAATTT  
CGTTATGCCCCAAGATGACTTTGTCTGGATCATAGTGAATGTGCTGTCTGAAGTCATCT  
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC  
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC  
CGTTGCATAAGTCCTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT  
GAGAAATACAAAATTGGAAAGGTCAATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT  
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT  
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT  
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGATGGAATTG  
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT  
GGCAGTGCCATGGTGTACAACCTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC  
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG  
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC  
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG  
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTGTGGATTCCCACCATTC  
CGAAGTGAGAACAATCTCCAGGAAGATCTTTCGACCAGATCTTGGCTGGGAAGCTGGAG  
TTTCCGGCCCCCTACTGGGATAACATCACGACTCTGCCAAGGAATTAATCAGTCAAATG  
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG  
TCAGATGATGCCTCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAAACAG  
CACTTTAATAATGCGCTCCCCAACAGAACAGCACTACCACCGGGTCTCCGTTCATCATG

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FIGURE 2R

GTGAGTGGAAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA  
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA  
AGATTGGCTTGGCATGTGGAGGGCACTCATTCGGCAACTCCCAGGCTTTGGGCACTGTGT  
GGAGGGGCTTGTGTAGGGACCAGAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC  
CTGGCTGGGCCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA  
CTCCCCAAGCCCTGGAGGGGTGTGTTGTGTTAGGAATTAACCTCCCTGCCTACCCCAAGGCC  
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA  
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTATAAAACACAGTTTGGGGCTTT  
TAAAGGTACATAATCAAGGAAAAAATATATATTATTTTTCAGGGTTGGTAACATTTTA  
TGAGATGTCAGTGACAACGATGGCCTTATTTTTCAGCCTTTTCTTCTCCAAAATGTT  
TCTTAAGGCAACTCTCCTAAATACATAAAACACAACAAATTAATGAAGAGTGACATGAG  
AGTAAATGAATCAAAAGGAAAAAACATTGAACCCAGAGGTGAGGGCAGCACACCCGAGCA  
GCTGTCCAGGCCTGAGCCAATGCAACCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT  
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCCAGGAGCAG  
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTCGAATCA  
GACCTGCCAAGGTGATGGGCGTCTGAGTTTACATCTGGGCCCCCGTGACCCCACTGAG  
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCCTGACTTGGGACAGGCCT  
CTCATCCTCTGGGAAGGTCTCCTTGTCTTCTACCCAACTAGAAGGGAAACAGTGGCATA  
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA  
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCCACTCC  
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCACTCCAAATATCTCAT

SEQ ID NO: 25\_W30246\_M SGK324\_M

ACCAAGTCCTCCAGCTCCTCTCCAACCAGCCCGGGAAGTTTCAGAGGATTGAAGATTTCT  
GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCCTGAACTTGACCGTTGCCTGAGC  
CCTGAAGGTGGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA  
ATAGGGAAGGTTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCGTGGACAGGTAC  
ACTGGAAGAGATTGTCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT  
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG  
GTTGAAGAGATGGAAACAGCAACTGACCTCTTCTAGTGATGGAAGTGGTCAAAGGTGGA  
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG  
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC  
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG  
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCAGGCCA  
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG  
GCAGCTGGTGTGATTACATACATACTTCTCTGTGGATTCCCACCATTCCGGAGTGAGAAC  
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATCCCAGCCCCC  
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG  
CCCGTGGGCTTCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG  
TGTCATCTCCAGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC  
CGCGGGGACGGGGGATGGTGTCTCCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC  
TGGCAGTTTCCCTGTTTTCCACCACCCCACTCTTTTAATAATTGTATATACTGTACT  
TGTTCTACTTGCTTGTCTTTAAACAGGGGCCCCACAGTTCACTCTCACTGTTAGATTT  
TGCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26\_AA383293\_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG  
CTGGTGGTGAATCAACGCCGCTTCCCCACCATGGAGGCCTTCTCTGCGAGGTGACATCA  
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTATGGCCACCCTGTG  
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTTGAACGATTC

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## FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA  
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAACTGTGTTG  
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG  
GGGCTCCCCTGTGTGAGCAGGGAAGGAGCTGGTAACGGCCATTACTATGTGGCTGTGCGA  
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA  
GGCAATGAAGCCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT  
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG  
TCAGAAACAAGCAGAGACGGGCAATCATTTCCCATCAGGAGTTATAGGAGTATATGGAGCT  
CCCCACCGAAGGAAGGAGACAGCGGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG  
ACAGAGGAGCCCTTGGATCAGAGGGCAGCACAGATAGTGAACAGGTTACTTGTCTGCAA  
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTCTGTTATGCC  
CAAGATGACTTTGTCTCTGATCATAGTCGTGACGGCTCCTGAGAGAGCACCAGGCGGGC  
TTTGAGAAGCTCCGAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA  
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG  
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCCAGAGCGGCCAGCGGTGCGAAGCCACGG  
CCCATGGGCATCATTGCCGCCAATGTGGAAGAGTGCAGACACCGGAGACCAGGCAGGCCTATGCG  
GATGGGAACCTTTGCTGTCTGTAAGGAGTGCAGACACCGGAGACATGGTGGACAGTGAGATC  
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC  
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA  
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC  
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA  
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGACCTCAAGCCGGAAAAACCTT  
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA  
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA  
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCTC  
TATATCCTGCTGTGTGGCTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG  
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCTTCCCCCTTACTGGGACAATATC  
TCTGATGCTGCTAAAGATCTGGTGAGCCGTTGTGTTGGTGGTAGACCCAAAAAGCGTAC  
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG  
AAACGACAGAAGCAGGTGTCCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAGAGG  
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCAGTTCTGCTC  
AAGGACAGAGAAAAGGATAGAAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA  
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAATAAATTAAGT  
CAATGTTAAATGTCAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATAACATTTT  
TGGGGGGTAAGCATTGTCTCAGTGAGGAATTTTGGTAATAATGATGTGTTTGTCTTCCC  
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC  
CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28\_AA197883\_M  
ATGCCAACCGCGCCGGTCTGTGCGCCCGCCGCGCCAGCGACCCCCGCCCCGCGGCA  
CCCAGTCGCCCCTGCGCCTCCCATTCGGGCCACCGAGGCCCATGTGACCATTCTCTGAAA  
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA  
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTGATGCCGCTGTTACGCCCT  
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCAGGGTGGTGACG  
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCCTGCTCCTCAACCGGCGCTCA  
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG  
AAGAACGACCGTGTGCGGAAGCTGTTACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT  
GACTTCTTCCGGGAGGGTGATGCTTTTATAGCTATGGGCAAAGAGCCGCTGACATTGAAG  
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCGGGCTCTTGCCCTGGCCCCCT  
CACAGTAGAGTCCCCCTCCCAAGGCTGAGAAGCAGACTTCCAGCAAGCTTCTGAAAGGA

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FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT  
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAAG  
TGGGTAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCCGCTTCACCCGGGGCAGCCACT  
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCT  
GGGAGATTGTGAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG  
AGGGAGCCGTGCCCGCTGGGAACCAAGAGCTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGAT  
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCCAAAATTTACAGAT  
GGAGAGGAAGGGTGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA  
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC  
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA  
GAGGAGGGGCGGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAGCATGCC  
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG  
GAGAAGCAAGCAGAGCAGGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG  
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG  
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT  
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC  
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGACAGTGTAG  
ATTTTAATCATCCAGAGTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA  
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTGATGCC  
ATCGTTGAAAATGTGAAGTTTCCAGAGCCGAGGCTGCAGTTATGATCACAGACTTGTGT  
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC  
CTCCTGGTTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG  
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT  
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC  
CTATACATCCTCTTGTGTGGCTTCCCCCTTCCGAAGTCTTGAGAGGGACCAAGACGAG  
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCCTCTCTCTTACTGGGACAACATT  
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC  
ACGGCCGAACAGGTCCTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG  
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACTTCCAGAGTCAGCACAAGAAG  
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29\_DRAK2\_H

CTCCGCTGCTGTGCCAGGAGTCACTTCACGAGAAGCCAGGTCACAACCGTCGGCCCTTG  
TCTGGAAGTAAGAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCGGCTG  
GAGCTAGAGAACTCGTCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA  
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGAATAAGAAG  
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTGATTGCCGAAGTATTTAGGC  
CTACTAACTACAACCTCTCAAATTTCAATAAAAAATGGAAAACTTTAATAATTTCTATATA  
CTTACATCTAAAGAGCTAGGGAGAGGAAAAATTTGCTGTGGTTAGACAATGTATATCAAAA  
TCTACTGGCCAAGAATATGCTGCAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT  
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT  
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAATCATTTTGATATTGGAATATGCT  
GCAGGTGGAGAAATTTTACGCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT  
GATGTTATCAGACTCATTAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC  
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCCTCTCGGG  
GACATTAAATAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACCTCGG  
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATACC  
ACAGCAACAGATATGTGGAATATTTGGTATAATAGCATATATGTTGTTAACTCACACATCA  
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT  
TATTCGGAAGAACTTTTTCATCAGTTTTCACAGCTGGCCACAGACTTTATTACAGGCCTT

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FIGURE 2U

TTAGTAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA  
CAGCAGTGGGACTTTGAAAACCTGTTTTACCCTGAAGAAAACCTCCAGTTCCTCTCAAAC  
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC  
TGTGGTGTAGAGAAGACAAAGAGAATATCCCAGAGGATAGCAGCTTGGTTTCCAAAAGA  
TTTCGTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTCAGATTTGCTCTGTTAG  
CACTTTTTTCTTTGACTCATTGGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT  
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA  
ATTTAGGGAAGTGTTTTAAATGTTAAATTAAGTGTGCTAGCATGTTATGATTTTCATATCC  
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAGTAAATTGTACAT  
GTGAAAG

SEQ ID NO: 30\_W44160\_M\_DRAK2\_M  
CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG  
GTCGCCGCGGGAGTCGCCTCACAGGGGCTGGCTGACGGCGACCAGCCGTGTGGGGAA  
GAGTGCAGAGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA  
GGAGATTCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA  
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAGAACTGGGAGAGGAAAAT  
TTGCTGTGGTTAGACAATGTATATCAAATCAACTGGACAAGAGTATGCTGCCAAATCCC  
TGGAGCTGGCCAGGTCTTGTCCCCACGTGATTAATCTGCATGAGGTCTACGAAAATGCAA  
CGGAAATCATTTTGGTGTTAGAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC  
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG  
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA  
TACTTTTGTAGCAGTATATACCCACTCGGGGACATAAAAATTTGTAGATTTTGGAAATGTCTC  
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC  
CAGAAATCCTCAACTATGATCCCATTACCACAGCAACAGATATGTGGAATATTGGCATAA  
TAGCGTATATGTTGTTAACTCATACATCACCATTGTTAGGAGAAGATAATCAAGAAACAT  
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC  
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCAGAGAAAAGACCAACAG  
CAGAATCCTGCCTATCCCCTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTCATC  
CTGAGGAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA  
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC  
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTTCGATTGCTGACTCCTTGGCCAGCCCC  
ATGAACTTGTTCAGATTTGTTCTGTAGCATTCTCTGTGACTCATCTGGACTGACT  
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT  
TATAAATGCACTTCTGCTTAGAAGAACTTAAGGAACAGTTAAATGCTAGGCTTCTGTTG  
GCTAGCATATCATTCTTGTCTGAAATTTGTTTGCAGAGGAAAATATTTAAGTATATGA  
CAAAAAATGTAAATTTGTGTTTAAAGAGAACACATGCAACTGAAAGAACTCAAGTTCAGTCA  
GACTTATAAAATGGGTTATATTATGGTTAGTAAAGTTGAAAAAAATGAAAACAGGAAT  
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA  
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA  
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT  
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGTTGATCCAGGCTGTTTCTC  
TGCAAACCGAGTCAAACTCGACATCATTTCCAGCTCATGTATTTTGTACGTGCATCATA  
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCTTGTCTTCTAGA  
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA  
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTGGATGTCTCCTAAGTCT  
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATCTTGTGTGAAATCTAG  
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA  
CACAAACATGGGAGTGTTCAGTGTGTCCGTGGTCAATATCTATGTTTCAGTCCTGATGG

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## FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAAGGTCTGTAATA  
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA  
ACAAATTTAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA  
ATTGTTACTAAAATTCCAAATTCFTTAGATAACTTTAAACTATTTAAATTGAGCATTGCT  
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTATTATTTTAAAGGAAAAGTTGT  
TTGCCCTTTTGATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT  
GATAGATAAAATACAGCCTTTAAACAACCTC

SEQ ID NO: 31\_H01248\_H, DRK1\_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG  
GGCCGGGCAGGCCGGGTCTGAGCGGGCGGTGCCGGCGCGCCGCCCGCCAGGCCCGC  
GGGCTGCTGACAGAGATACGCGCCGTGGTGCGCACCGAGCCCTTCCAGGACGGCTACAGC  
CTGTGCCCGGGCCGGGAGCTGGGCAGGGGGAATTTGCAGTGGTGAGAAAATGTATAAAG  
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAAGAAGAAAAGGCCAAGAT  
TGTGCGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG  
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT  
GCTGCTGGGGGTGAAATCTTTGACCAAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA  
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTTACACACTCGT  
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG  
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC  
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA  
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTAAACATATGTCATGCTTACAGGAATA  
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA  
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA  
CTTTTAGTTAAGAAACCTGAAGATCGAGCCAGTCTGTAAGAATGTCTAAAGCACCCCTGG  
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA  
AATGCCCTCCAAGAAGGTCAATTCTGTGCCTGAAATTAATTTCGGATACCGACAAATCAGAA  
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA  
TGCAGACAGTCTGAAAAAGAGAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT  
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32\_AA021445\_H

CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGCCCCGGGGCCGCCTGCTGCCTCCGCC  
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCTGCGGGCCGGCCAGCCGCTCC  
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCGTATCGGCTACTACGAGATCGACCG  
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC  
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT  
TTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCATATCATCAGGCTCTACCA  
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT  
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTGCGAAGTTCAA  
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGAACATTGTTTCATCGTGATTTAA  
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTCAG  
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC  
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCCAAAGTGGACATCTGGAGCCTTGG  
AGTTGTCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA  
TCTGCGGGCCCCGCTGCTGAGTGGAAAGTTCCGCATCCCATTTTTATGTCCACAGAATG  
TGAGCATTTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA  
GATCTGCAAGCACAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT  
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCTC  
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

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## FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA  
AACCCCTGCGTCTCGGAGCACTTCTAGCATGCCCGAGCCCTGGCCTTTCAAGCACCAGT  
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT  
GATCAACCCAGAGAACCAAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA  
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGCGCTATTTGTCAATGAGGAGGCACACAGT  
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT  
TCCTGGAGTCAACCCCCAGGCTCCATTCTGCAGGTGGCCCCCTAATGTGAACTTCATGCA  
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC  
TCTCTACAGCCGCCCACGCTACAGCTGTTGAATGGAATGGGCCCCCTTGGCCGGAGGGC  
ATCAGATGGAGGAGCCAACTCCAATGCATGCCCAGCAGCTGCTGAAGCGCCACGGGG  
ACCCTCTCCGCTTGTCAACATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA  
GAGCTCAGACGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA  
AAGACATACTGGCCATGACCAACCTACAGCTGAGATCCCACGGACCTACAACGGCA  
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACTGGTACCTGATCAGCA  
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCTGT  
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGA AAAAAT  
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA  
CGGGGGGAGATTGATGAAAGAACCCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA  
GCAGGAGCAGCACCATCAAATTTCTCCAGCAACAATTCAGACTCTATCTGTCTCTCTCA  
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT  
CCAGAGGTTAAGGATTTCAGCCTTCAAGCCACCCCCCAACCACCCCAACAACCATCTCTT  
CAGGCAGCCAGTAATAGTCTCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC  
TGCACTCTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC  
TGAGAACTGTTCTCTCTCTCCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC  
TCAGTCACAGCAGGTACCATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC  
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT  
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTCT  
CAAGCAGCTGAGTGCTGACAGTGCAGAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC  
TGCTAACTACGACCAGGCGCATTTACACCCCATCTGTTTTCGGACCACTCCCGGGGTTT  
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCAAGCCCTGAAAGT  
CCCTCCACTTGACCAATTCCCCACCTTCCCTCCCAGTGACATCAGCAGCCGCCACACTA  
TACCAGTCCGCACTACAGCAGGCTGCTGTCTCCCACGCCGAGACTATAACAAGACA  
CCAGCAGGTACCCCATCTTCAAGGACTGCTTTCTCCCCGCACTTCCGTCACCGGCCA  
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGACAGCTCATTAAAAGGCAGCAGCAACA  
ACGGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT  
GAACCAAGGGGATGCGGGGAGTCTGGCTCCCAGCCTTGGGGACAGAGCATGACAGAGCG  
CCAGGCTTTATCTTATCAAAATGCTGACTCTTATCACCATCACACAGCCCCCAGCATCT  
GCTACAAATCAGGGCACAAAGATGTGTCTCACAGGCTTCTTCAACCCCGCCCCACGG  
GTATGCTCACCAGCCGGCACTGATGCATTGAGAGCATGGAGGAGGACTGCTCGTGTGA  
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAAGGTGGCA  
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCTGAATCTTTGCTAGGAAC  
TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAAGTGTGCAAT  
CAGTAAAAATAAGGTGCCAGCAGAGAGCCTGTATAGGGAAGTGCATGGATAGAAGTTC  
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCAGCCCCCTC  
CGTCCATGAGCACCAAGGCCCGGGCCCTCCAGAGACACCACAGATCCAGAACAGCGA  
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT  
TAGCTCTGCCCCGATGTCCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA  
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTATGAGCAGCCAGCA  
CCTGAGTGATGGCAGCCAGCATTTAACTCCTTGTCTATCCATCTACGTGTATTACAGA  
CATCTGCTCAGCTACAAGCACCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

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## FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA  
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC  
TGCTTTCTCACATTTGGTTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC  
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC  
C

SEQ ID NO: 33\_2R22-5-11\_H

CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA  
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC  
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG  
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAGGCC  
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCTGTGACCAGAAGGCT  
TATTTGCAAGTTTCTTCTTCCCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT  
TGACAGAAAGAGAAGCATGAAATGAAGGTGAGAGATGAGATCCCGCAGCAGGGACGTGGG  
GGCCTCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAATAG  
CAAACAGAAGCCTTTGTCTCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC  
TGGCCAGAAAGTTCTGGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT  
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG  
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCAGTTCACTGCCTTCTCTACTAAA  
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTTGAACCTGGGCACCTGTCTGT  
CCTCAGTTGGCATCTCCACCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG  
CTGAGATGGAGACGTGAGCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC  
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTCA  
ACCGAGAGTAGCAAGGAGGGTGAGGAGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA  
CTGACACAGGACATGTCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG  
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAAACTTCTCCCAAGTGAAGCTT  
GGGATTCACTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA  
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT  
CCCAACATCATCCGCCTTTACGAAGTGGTGAGACCCTATCCAAGCTGCACTTGGTGATG  
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAATAATAGCACTGAGGGGAAGCTCTCTGAA  
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC  
CAAATTATTATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG  
AAGGTGGGCGATTTTGGATTACGACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC  
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT  
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGAAGTGGCACCATGCCA  
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA  
CCGCCGACGTGTGAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC  
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC  
CCTACACCTTTGGAACCTTTCCAAGTGGATCCCAACATTTGTGCGAAACCGCACTCTC  
AAGGAAGAAGAAAATGAGGTCAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT  
ATTCGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT  
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCAGTCATGATGCTACCAGAC  
CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC  
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACTAACCAAGATGATTGTT  
GCTGCTTCTAAATTTTTTCAAGGACAACCTGAGTGGAGACATTTTGTAAATTTTAAAT  
AACTTAAATTTGAGATATGCAAAAAAAA

SEQ ID NO: 34\_R31237\_1\_H, AAC33487

ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACCAACGTCA  
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

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## FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA  
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA  
GAGGTTGCAATAAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC  
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATGCCAATATAGTGAAGTTATTGAA  
GTCATTGAAACTGAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA  
TTTGACTATTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA  
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG  
GCTGAAAATCTATTGTAGATGCCGATATGAACATTAAAATAGCAGATTTTCGGTTTTCAGC  
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCCTCCATACGCAGCA  
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG  
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA  
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCCTTCTACATGTCTACAGACTGT  
GAAAACCTTCTCAAACGTTTCTGTTGCTAAATCCAATTAAACGCGGCACTCTAGAGCAA  
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT  
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT  
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA  
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC  
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT  
CCTCACCACAAAGTGCAGAGAAGTGTCTTCTCAAGCCAAAAGCAAAGACGCTACAGTGAC  
CATGCTGGACCAGCTATTCCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT  
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT  
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG  
GCGGATATTCTGAAACGCAAGAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT  
GGAATGACACGACGAAATACTTATGTTTGCAGTGAGAGAACTACAGCTGATAGACACTCA  
GTGATTGAGAATGGCAAAGAAAGCAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT  
ACACACAGTATCAGTAGTGACGCCACCCAGATCGAATCCGCTTCCCAAGAGCACTGCC  
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCGCAACATATAATGGCCCT  
CCTGCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC  
TCCACTAATCTCTTTAGTAAATTAACCTCAAACCTCACAAGGAGTCCGAAATGTATCTGCT  
GAGCAAAAAGATGAAAACAAAGCAAGCCTCGATCCCTACGCTTACCTGGAGCATG  
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAGTGTGGAC  
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT  
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT  
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35\_W90839\_M  
AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCCGTTGCCGGAACCTCTATCGCTTCC  
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC  
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAG  
ATCATTGATAAGACCCAGCTGAACCCAGTAGCTTGCAAGCTTTTGGAGGTGATAGAGACGGAG  
ATTATGAAGGACTCAACCACCCCAACATCGTGAAGCTTTTGGAGGTGATAGAGACGGAG  
AAGACGCTATACCTGGTGTGGAATACGCTAGCGCAGGAGAAGTGTGACTACCTCGTG  
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTACGCC  
GTGCACTACTGTCATCAGAAGAACTTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG  
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTACGAATGAGTTACGCTG  
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCAGAGCTGTTCCAG  
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCTCTGTACACG  
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGTGGGGAGCGAGTC  
CTCAGAGGAAAGTACCGGTCCCTTCTACATGTCTACAGACTGCGAGAGCATTTCTGCGG

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FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA  
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG  
CGGATGCCGGGTTCGGAAAGCGAGCTGCAGTGCAAGTGGGAGTGGAAAGTCGAGGCTTGCCC  
CCCTCCAGCCCCATGGTCAGTGTGCCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG  
CGGAAGGACAGCACTAGCACCCCTAACAACTCCCCCCCAGCATGATGACCCGAAGAAAC  
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCCTTGTGTCAAATGGCAAA  
GAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCTGGCT  
CCCCCGTCAGGCGAGCGGAGCCGCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT  
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA  
CCCCAGCCTCACCCACGCTTGCCCCACGAGGCCGACCCCTGCCCTCCGGGCGGCCTCGC  
CCCACCACCAACCTCTTACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA  
CCTGAGAGAATCGGGGGACCTGAGGTCAAGTTGCCATCTACCTTGGGATAAAACGGAA  
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC  
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

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GTAGCCGGCTTGGCGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT  
GGCCTCCCTTCTTCCCATGGAGGTTCGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG  
CCTTTCCAGAGCCTCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC  
TGAGCCCAGCAGGTCTTTTCTCAGCCCACAGACACCTGAGCAGAAGGAATGGGCTTTTC  
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC  
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCTGAGCA  
CACGGACCCGTCCGAACCGGGGAGTGTGTCTCTGCTGCTGCCCTGCTGCCGGGACTGTC  
CTCAGGGTGGTCTCACCTCTGCTTCCGGCCCCCTGTGTGCAACCCCTAACAGGCCATCTT  
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT  
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTTCTTTCTGAGGTGAGA  
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGGCCAGCGCCACGCTGCGGT  
GGTGTGTTGGCACGGTGGTGGACATCATCCCCGTAGTGGGGAGAAGATTCCAGTGTCTGT  
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTGGAGCCCGT  
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTCATGTGACAG  
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGGTGGGCAGCATATCAC  
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA  
GATTGAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT  
GAAATCCCAACCCAGCAGCGAGGAGGCGACACCGGTGAGGCGGCCCCCTGTGAGCGGCTA  
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGATGG  
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAGACGGA  
GCTCCTGGGCAAGAATATCACTTTCCTGATTCTGCTGTTTCTACAGCTACATGGACCTTGC  
GTACAACAGCTCATTACAGCTCCAGACCTGGCCAGCTGCCCTGGACGTCGGCAATGAGAG  
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA  
GGATCCAAGGATTAATGTCGTGCTTGTGGTGGCCACGTTGTGCCCGAGATGAGATCCG  
GAAGCTGATGGAAAGCCAAGACATCTTACCCGGGACTCAGACTGAGCTGATTGCTGGAGG  
CCAGCTCCTTTCTGCTCTCACCTCAGCCTGCTCCAGGGGTGGACAATGTCCAGAAGG  
AAGCCTGCCAGTGCAAGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG  
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC  
TGAACAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC  
TGAGGATGGGGCAGTGTGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG  
GATGGGAGTCAGTGGTCCAGCGGTTAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC  
CCAGGCCAAGGGTCAGCTGGCGGGGGGAGCCTCCTGATGCACTGCCCTTGCTATGGGAG  
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTTGGGATGGCAGG  
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

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## FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCAGTTGAGCCTTGACAGGAGCCCT  
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTACCGCTCCTGTGTCT  
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG  
CTATGCCTTGGCCACGGACCTCCCTGGGGGCTGGAAGCAGTGAGGCCCAGGAGGTTGA  
TGTGAATTCTGTTTTCTGGAACCTCAAGGAACCTCTTTTTCAGTGACCAGACAGACCAAC  
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT  
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTCTTGGATGACAG  
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCCGGGA  
GAGCTGTGTGGACATGATCCAACAGAACCGCTTGAGGTTTGTGTTGGTGTCTCTGAGCA  
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTCTTCCACGTTGGATGCTGGCCC  
TGAGGACAGTGGCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTCACCTCCACGCC  
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGAGATCCAGGAGGGTGCCTACTC  
CGGGAGCTGTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT  
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAGACCTCCTCCACAG  
CCAACGCGACTCAGCCGCCAGGACCCGCTGTTCTTCCAGCCTGCCCGGCTCCACCCA  
CTCTACCGCTGTGAGCTCACCAGACCCAGCCTGGTGGAAAGTGCTCAGAGCCAGACCTG  
GTTTGAGGAGCCCCCAAGGCTGTGGAACGGAGGGTGGCGGCTGTGAGGGCGAGTA  
CTCCCAAAGTACAGTACCATGAGCCGCTGGGAGGGTGGCGGCTTCGGCTTCGTGTGGAC  
TGCTGTGGACAAGGGAACCAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT  
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTGGGAAAGTTACTTTAGAGATCGCAAT  
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG  
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA  
CCGCCACCCAGGCTGGATGAGCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG  
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCAATCAAGCTGATAGACTTTGG  
CTCGGCCGCTACTTGGAAAGGGGAAATATTTTATCTTTTGTGGGACCATGTGGTC  
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC  
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA  
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT  
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA  
CCCGTGGGTAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT  
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGACCT  
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCAGCTAAACACCAATTC  
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCGTCTGCTGACCAGCTAAACACCAATTC  
TTCCTGCTTTTCTCCACTTGGTTTGGAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGGATGAGCCCCTGGCGAGTTTCATCTTTGACAACTAG  
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA  
ACATTGTGATTGCTGAGGACTTCAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT  
TAGAGAGGGGCAAACTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG  
TTCTCATTGGAAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTCAACC  
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG  
TTATTTCATCCCCATTCCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGAAGTGTGC  
AGCCTTGGCCTGAGCAGCGGACCACTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC  
AGCCTGTGAACCTTGTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA  
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC  
AGAGAGAGGGTCTCTGTGGGCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT  
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG  
GGCAGTTGTATGGATTTCAGGGCTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

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## FIGURE 2BB

TGACTTCTGCTTCTAGATTCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT  
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTATAACCTTGAAAATCATTCTAATG  
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG  
TGTTTAAGTTCTCTATTTTTTGTGTTTGTGTTTGTGTTGTAAGTTTTTGAGACAGGATCTC  
ACCATGTAACTTTGGCTGGCCTGGAACCAACTATGTAGACCAGGTAGACCTTAAACTGA  
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTACCATGCCCA  
GTTCTTCCTGGTTTTGTGTGTAGGTTTCTTCCCCTGACTTGGTACATGTGACATGTGA  
CAGATGTATGGAGTCTATAGAAGTGCCAGACAAAATGGCCAGAATATTTATTTATTTT  
CTTAAAAATTTCCAAATTAAAGCTACTTAGTTAACAGTTAACTGGCCAGGACTATATG  
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38\_AA785735\_H

GGCAGGAGGCGCGCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA  
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCTCCCGCCCCGCGCG  
CTCCTGTCCGCGGTGTCTAGCAGCGGGGCCAGCATGGTCATGGCGGATGGCCCGAGGCA  
CTTGCAAGCGCGGCGGTCCGGGTGGGGTTCTACGACATCGAGGGCACGTGGGCAAGGG  
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA  
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA  
AATAATGAAAATGTTAGACCACCTCACATAATCAAACCTTATCAGGTAATGGAGACCAA  
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAAATTTTACTATCTTGC  
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATCTGGCAAATCCTGTCTGC  
TGTTGATTATTGTCTGCTGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT  
GCTGGATAACAACATGAATATCAAAATAGCAGATTTTCGGTTTTGGAAAATTTCTTTAAAG  
TGTTGAAGTGTGGAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA  
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT  
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT  
TCTGGAAGGAAGATTCCGGATTCCGTATTTCTATGTGAGAAGATTGCGAGCACCTTATCCG  
AAGGATGTTGGTCTTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA  
ATGGATGCTCATAGAAGTTCCGTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA  
TGAGCCATCCATCGGGGAGTTTAAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAT  
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAAGAGCTATAACCACTTTGCTGCCAT  
TTATTTCTTGTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCAGTGAGCAGAG  
ACTTGATGGCCCGCCAGCGTCGGCCTAGCACCATTTGCTGAGCAAACAGTTGCCAAGGCACA  
GACTGTGGGGCTCCAGTGACCATGCATTACCGAACATGAGGCTGCTGCGATCTGCCCT  
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCAATTTCCAGCATCTGGCTGTGAGGCGGA  
AGCTGCATTCTAGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA  
CCCTGTGCCTCCTGTCTGTTGGGGAAGGGATGCCAGTCACTGCCCAGCAACATGATGGA  
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGGCCGAGGAAGACCCCGCTCATGC  
CTTTGAGGCATTTAGTCCACACGCGGCGAGAGACGGCACACTCTGTGAGAAGTGAC  
CAATCAACTGGTCTGTATGCCTGGGGCAGGGAAAATTTTCTCCATGAATGACAGCCCCTC  
CCTTGACAGTGTGGAATCTGAGTATGATATGGGGTCTGTTTCAAGGGACCTGAACTTTCT  
GGAAGACAACCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTACCCCCGATGAC  
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA  
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAAGAGGGGCCGAGAGCATCAGATAC  
CTCCCTCACCAGGGAATTGTAGCATTGTAGACAACATCTTCAGAATCTGGCTAGAACCAA  
AGGAATTCTAGAGTTGAACAAAGTGAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA  
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA  
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT  
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCCAGCCT  
TCTGTCAAAGGCCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

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## FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA  
ACTGCAGGCCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA  
GCAGCTGCCCCCTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG  
CCTGACCCAGCCCCTGAGCCCCCTCCTGGAGCCTTCCCTCCGAGCAGATGCAATACAGCCC  
TTTCCTCAGCCAGTACCAAGAGATGCAGCTTACAGCCCCTGCCCTCCACTTCCGGTCCCCG  
GGCTGCTCCTCCTCTGCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC  
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG  
TGAGCTGCCAAGCGCTGCTTCCCCCTGCGCCAGACTATCCCACTCCCTGT CAGTATCCTGT  
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCAGAAGCCCAGGACTGCA  
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG  
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCTGGTGAATTAGTCTCA  
GCACAGGAATTGAGGTGGGT CAGGTGAAGGAAGTGTATGTTCTTATTTTATTCAGC  
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC  
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGAGGCTGAGGCAGGAGAATGGCGTG  
CAAAGTTTTCTGTGGCAAGTGTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG  
AACCCGGGAGGCGGAGCTTGCACTGAGCCAAAGATCGTGCCACTGCACTCCAGCCTGGCG  
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC  
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT  
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGCGAG  
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA  
TTTTTGTCTTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC  
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC  
ACTGGGGCAGATAGAGAACCAGGCGGCAGCAGTGTCTCGCAGACCCACCCAGGGAGAGC  
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT  
TTGTACATTAGTTTTACCAAGCACTTCTCTTCTAACCCTCACAACAATTCTATGAAATT  
AGCTGGGGAGATACTGTCTTATTTTTTACAGCTGAAGAAACCAAGCTTTGGGAAGTTT  
GTGACTTCTCTGAGATCAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC  
TGGCTTCTGGTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTCCCTTCT  
CTTTCCTCAGTAGCATCTGACTCTTTTATAAGCAAACAGCTGTATAAACAAGCCCCA  
TTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA  
GCCGCTGGCTTTGGGAAGAGGCGCCTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG  
TGCACTGAACCAGGCTGAGGGAGACAAAACCCCGCAGACCCGCTGCCTTTCAGCGTCC  
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC  
AGCAGTTTCTTACAGAACACCCCTTCCCTCAATTGCCAAGGGCGCATCGCACGGCATC  
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCACTGAAGTCAAGCTTATTA  
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGGCCCATCAACTAGAAGTGCTTATTA  
CTTTTAGGATTAAGAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAGAGGCA  
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT  
ATGACCCAGATGGAATAATGTCACATTTCCCAAGTGCAGATAATGGGCTGCTGCTGGCTC  
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC  
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA  
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAGGGATACAGAGATA  
TCTGCACTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT  
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT  
TTTCTGTGTGCTTTTTTTTAACTAAGAAAAAATGGTGAGTTCACTAGCTTTGGTA  
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAATCAAAAGTATAACTTGTC  
ACTTAATGTTAGAAATTCCTAAATGCAGTGAATAAATAATCTCTGTACCAAATAGT  
AATTTAAATGGGTAATTTTCTGCAAGGAAATGTACTGTTTTTATGTTTCCAACCTCT  
TGA

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# FIGURE 2DD

SEQ ID NO: 39\_AA207220\_H

GCTGTGGCTCCCCGTCCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC  
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTC  
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCGGCCGCTGGCGGAAGGG  
CTGATCAAGTCGCCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG  
CACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG  
GTGAAGAAGGCGCGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC  
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTTCATCA  
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTGAGAACAGCAGCAAGATCGTG  
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG  
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC  
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT  
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG  
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC  
ACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC  
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC  
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG  
GTGAACCCACCCGCGCGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG  
GGCTACGCCACCCGAGTGGGAGAGCAGGAGCTCCGCATGAGGGTGGGCACCCTGGCAGT  
GACTCTGCCCCGCGCTCCATGGCTGACTGGCTCCGGCGTTTCTCCCGCCCCCTCTGGAG  
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC  
CCTGGCCTGGAGCGCCAGCATTGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCCAG  
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG  
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC  
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCCAGGGCAGGCTGCCCCCTGCTCCCCAAG  
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCCC  
AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG  
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT  
GGCAAGTTCTCCAGACAGCCTTGAGGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT  
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG  
GACAGCATCCTGTCTCTGAGTCTTTGACCAGCTGGACTTGCCCTGAACGGCTCCAGAG  
CCCCACTGCGGGGCTGTGTGTCTGTGGACAACTCACGGGGCTTGAGGAGCCCCCTCA  
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT  
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA  
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGG  
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCAGCTCAGA  
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG  
AAATGCGCCAAGGGTTGAGTGTCTGTCTTACGCCCTGCTGAACGAAGAGGATACTAAAGA  
GAGGGGAACGGGAATGCCCCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG  
GGCCACAGAGA

SEQ ID NO: 40\_AA426580\_H, MAK\_V\_H

ATGCCGGCGGCGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCTGGGGGCGGCGGG  
GGCGCGGAGGACGCGGCCAGGCCCCGCGCGGCCTGCGAGGGAAGTTTCTGCTGCTGCTGG  
GTGAGCGGCGTGGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCACAAGCGCGTGGGCAAC  
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGTCTCTTTGCCAAGGTGCGCGAGGGGCTG  
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAG  
GACACCTATGTCACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC  
CCCAATATCACTCAGCTCCTTGATATTTAGAAAACGGAAAACAGCTACTACCTGGTCTATG  
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

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## FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGCC  
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC  
AAGCTGATTGACTTTTGGTTTGAAGCAACTGCGCAGGGATCCTGGGTACTCGGATCCGTTC  
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAG  
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG  
CTGCCTTTTACGGTGGAGCCTTTTACGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA  
GAAATGAACCCCTCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC  
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTAGCAGGCACTGGCGAATCGCTGGCTT  
AATGAGAATTACACGGGCAAAGTGCCTGTAAATGTACCTATCCCAACAGGATTTCTCTG  
GAAGATCTGAGCCCGAGCGTTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC  
GACGTGATCAACACTGTGCTCTCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC  
TTAAACAAGAACTGGAGCGCTATTTGTGAGGAAATCTGACATCCAGGACAGCCTCTGC  
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC  
TCTCTGGACACCTGGACACGAGATCTTGAATTCATGCCGTGCAGGATAAAAAGCCCCAA  
GAAACAAGAAAAAGAGGGGATTTTCTTCATCGACCATTCTCCAAGAAGTTGGACAAGAAC  
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC  
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC  
CGCAATATTTTCCGCAAACCTCAGATTCCAATTGTGTGGCTTCTTCTTCCATGGAGTTC  
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA  
GGGCCCCGAAGCACTGGCATCCCCCAAGGAAGACCCCTGATGCTGGACATGGTGGCG  
TCCTTCGAGTCTGTGGATCGCGACGACCACGTAGAAGTGCTGTCTCCCTCTCATCTACTAC  
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCAGCGAGAGGACGCTGTCC  
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAATCTGGTC  
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT  
CCGGTCCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA  
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG  
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCTAGCCCCCTGTG  
AACCTTGCCCTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

SEQ ID NO: 41\_Z36720\_H  
ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA  
GATGTACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGCCCTG  
CACAGGCTGGAGGCCTCCCGGGCACCGGGCCGGGGCTGATGGGGTTCCCCACATT  
GACACCCAGGCTGGGTGGCCCGAGGTCTTGGAGCTGGTGAGGGCCATGCAGCAGGATGCG  
GCCAGCACGGTGCCAGGCTGGAGGCCCTCTTCAAGATGGTGGCTGCGGTGGACAGGGCC  
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTCATGCAGGGG  
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG  
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG  
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG  
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGGAAGAAGAGGGAGGAAAACCAAAGCAT  
GTGCTGAGCACCAGTGGGGTGCACTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG  
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA  
GCTGACCCCGCCAGGCAGTGGTCTACCGGGCCAGGGAGATGGTGTTCCTGGCCAGCC  
CAGGCATTCCCTGGCCACCTGCCCCCTGCCCAAAAGGTGGAAGCCAAGGCTCCTGAGACA  
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACC CGCAGGGTCAATGTG  
GTCTCCCCGAGCCTGGAGGTTGCACAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT  
GACCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGGCCA  
GGCCCTCAGGGCTGCCAGCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA  
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGT  
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATACAAGAGATGGATACTCCT

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FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA  
GCAGCTGCCCAGCCAGGCAAGCAGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT  
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCGCTGCAGGAG  
AGCAGCAGCCCCGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGGTGGGGCCGAGCCTGGC  
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG  
CAGCAGGGCAAAGCCCCAGGGGCGGGAAACCCTGAGCCTGAGCAGGACTGTGCAGCCAGG  
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCCAGGCGCCGAGGCTGGCAGCGTG  
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG  
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTCCG  
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC  
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC  
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC  
ACCTTGTCTATGGAGTACGTGGACGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG  
TACCACCTGACTGAGCTGGATGTGGTCTGTTCACCAGGCAGATCTGTGAGGGTGTGCAT  
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC  
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT  
CGAGAGAAGCTGAAGGTGAACCTCGGCACCTCTGAGTTCTTGGCCCCAGAAGTCGTCAAT  
TATGAGTTTGTCTCATTCCCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA  
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTATTGTA  
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC  
TTTGTTCCTCCGGTTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG  
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA  
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG  
GTGACTGCTGCCAACAGGTTAAGGAAATTTCCAACCTTCTCCCTAA

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GGGGAGATGGCGCTGTTTGAGTGCCTGGTGGCGGGGCCCCACTGACGTGGAGGTGGATTGG  
CTGTGCCGTGGCCGCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC  
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC  
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCCGGCTGACCGTGCGGCCCTCG  
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTGGAGGGCCGAGCTGCC  
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGAATCATTTTGGC  
TGCCCCATGGAGGAGAGTGAGAACTTGCGGCTGCGGCAGGACGGGGGTCTGCACTCACTG  
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTCACTGCTGTTAACACC  
CATGGCCAGGCCCACTGCTCAGCCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA  
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCCGAGGAGCCAGAGCAGGGTGAG  
CTGGAGCGGCTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG  
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCTGCCCTACCCACCATCAGCTGG  
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT  
GTCCATCGCTTGGTGTTCCCTGCCGTGGGGCCTCAGCACGCCGTGTCTACAAGAGCGTC  
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCCACCTGTATGTACAGATGTGGTC  
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACACTC  
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGAATCCCTGACGTACACA  
GTGCAGCACCAGGTGCTGGGCTCGGACAGTGGACGGCACTGGTCAAGGCCTGCGGGAG  
CCAGGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCCGGGTCCCTCAGC  
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGAG  
CACGGCCCAACCCTGGAGGAGGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG  
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGGCCAGGTGCTC  
TGGAGGAGCTGCCGAGGGGCCCTCTAGAGGCACGGGCGGTGTGTACGAGCTGAGCCAG  
CCAGATGATGACCAGTACTGTCTCGGATCTGCCGGGTGAGCCGCGGGACATGGGGGCC

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## FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCAACGGCACACAGACCTGCTCGGTACATTGGAGCTG  
GCAGAGGCCCCCTCGGTTTGTAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAACT  
GCTCGCTTTGCGGTGGTGGTTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC  
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC  
CTGGTGGTGTCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC  
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTGAGCTCAGACAGCTATG  
GAGGTGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT  
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGAGCGT  
AGCTCCGGCCTGGAGTTTTCGGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA  
GCGCGTTCGGGAGGCCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT  
GAGGCCTTCGAGAGGCGCCGGGACTGGTCAATTGTACCGAGCTCTGCACAGAGGAGCTG  
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG  
CAGGTGCTAGAGGGAATACACTACCTGCACAGAGCCACGTGCTGCACCTCGATGTCAAG  
CCTGAGAACCTGTGGTGTGGGATGGTGTGCTGCGGGCAGCAGCAGGTGCGGATCTGTGAC  
TTTGGGAATGCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT  
GAGTTTGTAGACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG  
CCTGTGGGTGTTGTTGCCTTCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAT  
GACCGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCATTTC  
CTGAGCCTGAGCAGGGAGGCCCCGGGGCTTCTCATCAAAGTGTGGTGACGAGCCGGCTG  
AGACCTACCGCAGAAGAGACCTAGAACATCCTTGGTTCAAACTCAGGCAAGGGCGCA  
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCGCGGAGGTGGCAGCGCTCCCAG  
ATCAGCTACAAATGCCACCTGGTGTGCTGCGCCCCATCCCCGAGCTGTGCGGGCCCCCA  
GAGCGGGTGTGGGTGACCATGCCCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCTCC  
TCGGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCACTGCAGCCC  
GAGTTCTCTGGCTCCCGGTGTCCCTCACAGACATTCCCACTGAGGATGAGGCCCTGGGG  
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT  
CAGGACCAGGAGGCTCCAGCCCCAGAGGCCCTCCCTCCCCAGGCCAGAGCCCGCAGCT  
GGGGCTAGCCCCAGGCGGGGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC  
CGGGCCGGGCGCGGGAGCTGGGCGGGGCTGCACAAGGCGGCGTCTGTGGAGCTGCCG  
CAGCGCCGAGCCCCGGGCCGAGCCACCCGCTGGCCCCGGGGAGGCCCTGGGTGAGGGC  
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGCGGTGCTCGGGAC  
GGCAAGGTGAGCGGCTCAGGGGTCCCTGCTGGAGAGCCTGGGGGCGGTGCTCGGGAC  
CCCCGATGGCAGGCTGCCTCAGCGAGGCGCGCCCCACACAGCCCCACTCGAG  
AACCGGGCCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG  
CACCGCCGAGCGGGGCGCCCCCTGAGATCCCCGTGGCCAGGCTTGGGGCCCGTAGGCTA  
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC  
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT  
GCTCCGCAGCCCCCGCACCCAGCCTGCCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA  
CCAGTCCGAGCCTCCAAGCCTGCACACCCCCCAGGCCCTGCAAACCTAGCGCTGCCC  
CTCACACCTATGCTCAGATCATTCAGTCCCTCCAGCTGTGAGGCCACGCCAGGGCCCC  
TCGCAGGGCCCTGCCGCGCGCCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG  
GTGGCCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGCCTCAGCCGGGGTCCCCCG  
GTGCTAGCCGAGAAAGCCCCGAGTTCACCGGTGCCCGCCAGGCCAAGTTCAAGCGCAGCCG  
AGCAGCATCGAAAACCTTGAGTCGGAGGCGGTGTTTCGAGGCCAAGTTCAAGCGCAGCCG  
GAGTCGCCCCCTGTGCTGGGGTGGGCTGCTGAGCCGTTGCGGCTCGGAGGAGCGCGG  
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCCGCGGGGACCCCC  
CTGGAGCTGGTGACGCGCTGAGCGCTCAGCTCGGTGCAGGACCTCAGGGCTGTGCGA  
GAGCCTGGCCTCGTCCGCGCCTCTCGCTGTCACTGTCCAGCGGCTGCGGCGGACCCCT  
CCCGCGCAGCGCCACCCGGCCTGGGAGGCCCGCGGGGACGGAGAGAGCTCGGAGGGC  
GGGAGCTCGGCGGGGCTCCCCGGTGTGGCGATGCGCAGGCGGCTGAGCTTCAACCTG

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## FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCC  
GGCCGCAGCACGCCGCTGTTTCGGACGGCTTCGACGGGCCACGTCCGAGGGCGAGAGTCTG  
CGGCGCCTTGCCCTTCCGCACAACCAAGTTGGCCGCCAGGCCGGCCACCACGCCTTCC  
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCCGGGCTCCTCAGCCCCAGGGGAAAGC  
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTATCGCCACCA  
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACCAGTACGTGCGCAGTGAGTCAGAC  
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGAGGCAGCC  
ACCCTGCTCTGCCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG  
AAGTCCTTGAGGTCAAGCCCTCAGTGATCATCGTGTCTCTGCAAAGATGGGCGGCAGCTG  
CTCAGCATCCCCGGGGCGGGCAAGCGGCACGCCGGTCTCTATGAGTGCTCGGCCACCAAC  
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCCAGTCCCAGGAAAGCTA  
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGCTGTGGAGCCGGGA  
GACAGCCGGGCACCTTGACAGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG  
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC  
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCGTGCTGGGCAGGGGCCCTTCAGCAAC  
TCTTCTGAGAAGGTCTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGTCTGCC  
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCCGGCCTCCTGACTCTCCTACC  
TCACTGGCCCCACCCCTAGCTCCTGTGCTGCCCCACACCCCCGTCACTGTGAGCCCC  
TCATCTCCCCCACAACCTCCTAGCCAGGCCTTGTCTCGCTCAAGGCTGTGGGTCCACCA  
CCCCAAACCCCTCCACGAAGACACAGGGGCTGCAGGCTGCCCCGCCAGCGGAGCCACC  
CTACCCAGTACCCACGTACCCCCAAGTGAGCCCAAGCCTTTCTGCTCTTGACACTGGGACC  
CCGATCCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGTCTTCTCTACTCCTGTGTAT  
GTGGTGACTTCTTTGTGTCTGCACCACAGCCCTGAGCCCCCAGCCCTGAGCCCCCT  
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCCGCCAAGGAGGTGGTCACTCC  
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC  
CCTCAGAAACCCCTACACCTTCTGGAGGAGAAAGCCAGGGGCGCTTTGGTGTTGTGCGA  
GCGTGCCGGGAGAAATGCCACGGGGCGAACGTTCTGGGCCAAGATCGTGCCCTATGCTGCC  
GAGGGCAAGCCGCGGGTCTGCAGGAGTACAGAGGTGCTGCGGACCCTGCACCACGAGCGG  
ATCATGTCCCTGCACGAGGCCTACATCACCCTCGGTACCTCGTGCTCATTGCTGAGAGC  
TGTGGCAACCGGGAACCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC  
GTGGCACTTACATGGTGCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG  
CTCCACCTAGACATCAAGCCAGACAACCTGCTGTGCTGGCCCCCTGACAATGCCCTCAAGATT  
GTGGACTTTGGCAGTGCCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC  
ACGGGCACGCTGGAGTTCATGGCTCCGGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC  
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT  
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCGCTTTGATGCCTTC  
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCTCTTCTTGCGAAAGGTTCTCTGTGA  
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC  
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTCACCACCAACCGGCTCAAGGAGTTC  
CTGGGCGAGCAGCGGCGGGCGCCGGCTGAGGCTGCCACCCGCCACAAGGTGCTGTGCGC  
TCCTACCCCTGGCGGCCCCCTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG  
TTCCCAACCAATGCCACGGGACATTCCAGGGCCCCACGCTGAGCCAGGCGGGCTGGGGCTT  
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA  
GACCCAGGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG  
TCAGGCTCAGCAGGTTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGAGAGG  
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTCACT  
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC  
CCAGGTGTGAGGTCAGTGGCTGGGAGTCAGTGTGGCAAAGCGGGGGCAGGACACAGATA  
CAGTGGCAGGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG  
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGCTGTGAGCATCCCTCAGAGGAGAAATGTG

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## FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCCTCCTGTCCAGTGGATACAGC  
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCCTCCATGGCCTTTGGCCTTCT  
TCCCATTCATATTTATTTATTTATTTACTTTTATGAAGTTTCCCCTTCCATCCGATCCCT  
ACTGCCCATGTTGTCCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA  
AGGAAATAAAAATGGCAAGCAGCAAAAAA

SEQ ID NO: 43\_AA542015\_M SGK088\_M  
GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA  
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTGCTTTGATGCC  
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCCTCTCA  
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCACCCATGGCTGCAAGAT  
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA  
TTCCTGGGCGAGCAGCGCGACGTGCGGCTGAGGCTGTACCCGTCAAGGTGCTGTCTC  
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCAGACAGCCGAGCCCGGCCACGGGCTTCAACT  
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG  
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT  
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTACCCCGGCCATA  
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAGA  
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT  
TAGGCTGGAGTGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG  
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC  
CAGGAGCCAGAGCAGAGACATAAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT  
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAG  
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCCAGCCGATGCAGTTCTGGGCGTTCTCC  
ACTGGCCAGGGATGTCTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCATTGTAT  
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTCCCTATGTTG  
TCCCGACCATCCCCCTTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTCACA  
AGGAAATAAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACACAGC

SEQ ID NO: 44\_R19772\_H  
ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG  
TGCTGCTGTTGCTTCCCCTGTAGAGATGCATACTCTCATTCCTCAAGCGAGAATGGAGGC  
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACTTCATCCACAGTTCC  
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCTGTGCGTCGG  
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTCGCGATGGTCGG  
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC  
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCAACACACCC  
CTCCACACCTATGAAGATTTTGAACAACGACCCTACACAGGATGAAATGTCTCTCTCT  
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA  
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATAACGGGGGAGCTTG  
AAAGACCCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA  
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA  
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA  
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTGTTGAAAT  
ATTCATCAGATTTATGACTGGCATAAGGATTTTTTCTGGCGGAACTGGAAAAGTGTATC  
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC  
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC  
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCTCATCAAG  
CCCATTGAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCTGAGATACAGTGAG  
AAGGCTGGTTTGGAGTGTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

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## FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT  
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG  
CAGTCCCGGACCAAAGAGAGGGCGGTGTTCTCTTCGAGCAGATTGTTCATCTTCAGTGAA  
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAAGGAGCATCAAGATGAAT  
TACTTGGTCTCTGGAGGAGAATGTGGACAATGATCCCTGCAAGTTTGCACATCATGAACAGA  
GAGACTTCTGAGAGGGTTGTTCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG  
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTGAATGCACTGCAATCGCCC  
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT  
CCCCAAGCCAGCCCCAGGCCCTACTCTCTGTTCTCTGCGGGCTCAGAGAAGCCCCCAAAG  
GGCTCCAGCTATAACCCACCTCTGCCTCCCTGAAGATATCTACCTCCAATGGCAGTCCA  
GGGTTTGAATACCACAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC  
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA  
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAAACATGTGT  
CTGGTGATACCAGCCTGCCAGCGACCATTTCCCCCGCCGCGAGGGCTGGGTCCCAGGCAGC  
ATCCTGGCGCCCCCTCACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG  
TCATGTTTATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA  
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTTAAA  
GAGACGAACAGTTCAGGAGGATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG  
ATCTTAAATCCAAATTTTATCCAAGAAGTGGCCCCAGAATTCCTTGTGCCCTTGGTGGAT  
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG  
CCCACCATCTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC  
ACATACACGGTCTCCTCTTGATGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG  
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCATCAACG  
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCAGGAG  
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT  
ATTTCTGGTTTACACTGTGGAGTACAGAGAGGAAGGTTCTCAGATCTGGCAGCAGTCAGTG  
GCTTCGACCTTGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCTTATCAG  
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCAGCGAGCCCTCGGAGTTT  
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTCTTGAAGGAAAAAT  
TTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG  
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTTAAACAAAAAATG  
AAGAAGAAAGAACAGGCTGCCCCAGGAGGTGCCCTGCTTCAGCACCTACAGCACCCCCAG  
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGAACTG  
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA  
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACTGAGGAGTT  
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA  
GTGAAGCTCATTGACTTGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTCACCAC  
CTGCTGGGGAACCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG  
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTATGCTGAGTGGGGTCTCCCCC  
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC  
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTATCAATGTGATCTTA  
CAGGAAGATTTTCGGAGGCGGCCACAGCAGCCACATGCTTGCAGCATCCATGGCTGCAG  
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA  
GAACGTCGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC  
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45\_5R72\_8\_2\_H  
CGCCGCTGTTTGTCTCGCGCGGCCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA  
AAGTTTCTCCCGGTGCAGAAATCCGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT  
GTCCGAGACCCGCCAGTCCGCGCGCCCCGGCTTTGTTTCGTGCGGAAGTGTAGTGGTGAGA

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## FIGURE 2KK

AAAACTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC  
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAAGTTC  
GAAATTACAGTTTTTACCATCACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCTCCTCAA  
CAGTGGAAACATTTTTAAAGTTGCTTTTGTGTCAGAGTTAAACAAATGGCTGATAGTGGC  
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT  
TGTGTATGTTCCAGCAAAACAAGGTTTCCCTCCAGTTTGGTGGTGAAATGTACAGACA  
TCAAGCATTGGTAGTGCAGAACTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC  
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA  
GCATCTCAGCAACAATGGGGTTCGGGGCACTTTACAGAAGGAAAAGTTCCCTCACATAAGG  
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG  
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAA  
AAAGTGAAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC  
ATTCTGAAAAGTGTAACACATGAACACATCATCTGGAACAAGTATTTGAAACGCCA  
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAACTCAAAGAAATTCTGGAT  
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT  
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG  
GTTAAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT  
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG  
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGCACGACTATAGCCAGCAGTGTGAC  
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCCTTTTTGGCA  
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA  
GTCTGGAATTCCATAAGTGAAGTGTGCTAAAAGTGTGTTTGAACAACCTTAAAGTAGAT  
CCTGCTCAGAAATCAGAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA  
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA  
GAAAGTGTGAGGAAAAACACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG  
AAAAGTTACCAACCCTGGGGAATGTCCCTGAGACCAATTACACTTCAGATGAAGAGGAG  
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCCCTGCAACCAGTAAGGCAACTTTGAT  
ATGTGCAGTTCAAGTTTCACATCTAGCAAACTCCTTCCAGCTGAAATCAAGGGAGAAATG  
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC  
GCCCTGTCCAGAACCAAAAAGAACTCTAAGGTTCCCTCCAGTGTGACAGTACAAAA  
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG  
CTGAGCTTGTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTGCACCAGCTTAAAT  
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG  
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG  
GGGCGAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTACTTCAATTCT  
TATGTTTAGGCACAGCTATTTATAGGGGAAAAACAAGAGGCCAAATATAGTAATGGAGGTG  
CCAAATAATTATGTGCACCTTTGCACTAGAAGACTTTGTTAGAAAATTACTAATAAACTTG  
CCATACGTATTACAGCAGAAGTGCTTCAGTCATTACATGTGTTTCGTGAGATTTTAGGTT  
GCTATAGATTGTTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG  
CTTGCCATTAACTTGCTGCTAAATTTCCCAATGTATTGATTAAATCAATAAAAAACAGATG  
TTACTC

SEQ ID NO: 46\_SGK309\_H  
GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCCTAGGTAGATGGCCCCCTCAGG  
GCAGGCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT  
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC  
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAGATC  
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCCAG  
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTCCGGC  
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGCTAAGAGAGGGGAAGGAC

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## FIGURE 2LL

CATGTGTGCAGGTTCAATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG  
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG  
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGGAGTCCATCGAGGCCATCCACTCTGTG  
GGCTTGCTGCA~~CG~~GTGACATCAAGCCTTCAAACCTTGCCATGGGCAGGCTGCCCTCCACC  
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG  
GATGTGCGGGCCCCCTCGGAATGTGGCCGGGTTTTCGAGGAACGGTTTCGCTATGCCTCAGTC  
AATGCCCAACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG  
CTGGTGGAGTTTGCAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA  
GGGATGATCAAGGAGAAGTATGAGCACCGGATGCTGCTGAAGCACATGCCGTGAGAGTTT  
CACCTCTTCCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCCGACTACCAGTTG  
ATCATGTGAGTGTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT  
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA  
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG  
GGACCTGCTCCGGGAGAACACCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAAGGA  
GAATGCACCCCCAATTCTGCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT  
TGTCCCCACCCCGGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA  
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT  
TTTCTCTACCCCCGATTCCCAGCCTTGTGCCCTGCCCTGTTCTCTCCTAAGCACCTGT  
CCCCCGCAATCTCCTGCTTGCCCGGCCTCTGTTTCCGGTCCCTCCCCGGCACTAGCC  
TCGCTGTGTCTTCCATCATCATCATCCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47\_AA234451\_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG  
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC  
AGCAGCCGCCCGCCGCCCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG  
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCCCGCAGTCCGCGGTGGGGGATGGGCAGGCA  
GTGGCGGTCCCCGCTGCCGAGGGTTAAACCCCGCCGGTCCCGGTCTGAGCTGGACCAGA  
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCCAGGTTAAATGGAAACCACCTTGG  
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA  
GAGCAGCTGGATATCCTGAGTGTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA  
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA  
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT  
GCTGTTTTGAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG  
AATGATCGATTCAACTATGTGGTCATGCAAGGTGCGAGGTGCGAATCTGGCAGATCTTCGC  
CGTAGCCAGTCCCGAGGCACATTACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT  
TTGGAGTCTATTGAAAGCATTCACTCTGTGGGATCTTGNATCGAGACATCAAACCGTCG  
AACTTCGCTATGGGTGCTTTCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC  
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTGAGCCACCTCGAGCTGTGGCAGGT  
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA  
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC  
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG  
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG  
GATTATTTTACAAAACCACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG  
ACTTTTGGAGTAATTGAGAGTGACCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC  
CTAACAACCACTACTTCTACCAACCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA  
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG  
GTATTTCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA  
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG  
ATGGATGCCAACAACAAAGATAAAGCTTGAATTTGTAAGGCTGCTACTGAAGAGGAG  
AACAGCCATGGCCAGGCAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTTCGT



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## FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTTCCACTGGTGCGAAAGTTACGTTCC  
ATTACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG  
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTCTTTTAAAGCTTCTAAGGTACCATT  
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTTACATAAAGTCTTTCAAA  
TAAGAAATCCTTGCAATTTTGTAACTGAGTCTATTTCAGCTCCAATTTTCATCCATGTT  
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT  
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT  
TTTTACAGTAACTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG  
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT  
AATTACATACACAAGGGACGGTGAGTTCAATTCACCTTTAGTGAAGACCTCTAGGAGTAAG  
ATACTGTGGGAAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC  
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG  
TGCATGGTTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48\_AA435956\_H  
ACTTTTACTATATTCTTTGAGATGACTGTTTTTGATTTAGAGGCGAAATCAGCACGTGGT  
GGCTCAAATCTCCTTATGGATAGTGTTCCTTCCTCCAGCTTTTCATGTTCAACTTTTG  
CGGGGCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC  
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG  
TCCATTCCTCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT  
GCTTTGCTGGGAGCCACTGAATATTCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC  
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGGGGTTTCCAACATCCTTGAACAG  
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC  
AAGCTACCTAACTACAATCCAGAATGGTTCCTGAGCTGAAGACCTGGCCTCCAGATGCTAAAA  
GTCTGGAACAGGCTGGGCAGGGTTCCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAA  
GGCTTTCCAGAGACCGCGTCTCCGCCCAGGAAGCACTTGTTTATGATTATTTTCAGCGCC  
CTGCCATCTCAGCTGTACAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG  
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCACCAAGGCTCTT  
CAGTTTAGCAAATGCTGGTGAAGAAAGGGCGAGATCACCAGGTTCTTCCAGGGCTGT  
ATTTCTGCAGTTTTCGGTTTTTCACTTTCAGCTTACTAAGAAGCTTCAAATCTAATCC  
ATACTGAACAAGGGGCTTTATGTCCTCACCTATGACCTGGAATAGTTTAAATATGGTGT  
CAAGGCAATAGTACATAATAGTGGAAGAAATTCAGTGGAAGGTTATTGCTATTGTCATT  
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAATAAGTCTAAGAAG

SEQ ID NO: 49\_AA626859\_H  
AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA  
TTTCTGTATATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC  
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA  
TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTGTGGGAGA  
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTGTCAGAGCTCCT  
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG  
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA  
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGT  
TCATCCTGTGGCTCTGAACCTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT  
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTA  
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT  
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA  
ATTTGATCACCTTCCAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT  
GTACACATTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

**FIGURE 2NN**

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCTTTCCCCA  
TGCTTTTACAT

SEQ-ID NO: 50\_AA061797\_M

GAAAATAGCCCTGCGGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT  
CATCGAGTGTTTCAGAAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC  
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAGTGT  
GCTATGGCAAACCTTCAAGCCCTTAACCTTCTGTACAAGACAATTGTATTCATCGGGA  
TGTAACACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG  
ATTTGCACGAATTCTAATTCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTGGTA  
CCGAGCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC  
CGTCGGCTGTGTTTTGTCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAATCCGA  
CGTGGAACAGCTTTACCTGATCATCAGGACGTTGGGGAAGCTGATTCCAAGACACCAGTC  
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACGAGGACATGGA  
GACTCTTGAAGAAAAATTCTCAAATGTTTCAAGCTGTGGCTTTAAGTTTCATGAAGGGATG  
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCAGCTGCTGGACAGTGCCCTACTT  
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCGCAGTGAGGGGAGAACCCGAAG  
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCTGGAAGCCACATCTCCCCACACCTGA  
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTTCGATCATCTTCCAAACATTTAGGGGACTCA  
TCCTTCCAGCACATCCTTTTAAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA  
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC  
CTGTGCTTTTTTCCACGCCAGCTCCATCTCTTAAACATTTCTTTTAAATGTTGCAGTATC  
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTACCAGAGCCGGGCTTCTCAGGCAA  
TCGGTACTGTGCATCTGTGGAATTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT  
CTCACTTCAGCCGACCAGTGGTGTCTTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT  
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT  
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT  
TGACTCCACAGCAGATGCTAGTCTCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA  
CGAACTAGAGAAAAATCCAAACGTGACCAGTTAGTGACAGACTACAAGGAATCGACCAC  
CATAACACAGTAACGCCCCTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT  
CACCATGGTTTTCTTTTCTTTTCTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC  
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAAATCAAAGACAAGCAGGAGGCCAGCCTAAG  
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCAAGTCCCT  
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCAATTG  
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTCTAAATATTCTCCACACTGGTG  
AGTATCTTGGCATTTCATTTCTGACCTCATCAGATGAACACATCAAAGGATGAGTATG  
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG  
GGGCCATAACTGAACCTGTGGAGTTCTTGCTGTGTCAGGAAACCCCTCTGGTTTTGTCT  
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT  
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG  
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC  
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAATAAGGAGTCGTTGAAGGTAG  
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTGTAGTATTA  
GCATTAATGTATGTAGAAGCTGGGCTATTTAGATTATTTGAAATTGTAGCTATTGTTAA  
TTAGCACTTAATAACTAAGTATGTTAGTCTAACTATTAGAGTTTACTACAAAG  
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA  
GAAAGCTATATAAGATTAAACATTTTTGTGGCTGTATATTGTGTATATACCTGGTTG  
TTCTTTAAATATTTTAAATAAAAGCCAGAAACATT

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## FIGURE 200

SEQ ID NO: 51\_AA397553\_H  
ATGCCCAATTTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGAAC  
TTGCAGCCGTTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG  
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCCGAAGCA  
GCATCCCTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC  
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT  
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCCG  
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAAGAGTCTCCAGCAAGTCG  
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTTGAATGAGGAGACTGATGAC  
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCATCCAAGCTCCAC  
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT  
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCCAAACCGGAGATCC  
AGGAGCCCCCAGAGGAAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCCTCGGGAGCT  
TCTTATGGCCAAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC  
TCCTACAAGAAAAAGTCTTGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG  
GAGCCTTCGGCCTACCAGTCCAGCACCCGGTCACCGAGCCCCCTACAGTAGGCGACAGAGA  
TCTGTGAGTCCCTATAGCAGGAGACGGTCGTCCAGCTACGAAAGAAGTGGCTCTTACAGC  
GGGCGATCGCCAGTCCCTATGGTGAAGGCGGTCCAGCAGCCCTTTCCTGAGCAAGCGG  
TCTCTGAGTCCGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCCT  
GCATATTCAAGACATTCTCTCTCATAGTAAAAAGAAGAGATCCAGTTTACCGCAGTCGT  
CATTCAGTATCTCACCTGTGAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT  
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGTCAGCAAAGATGGATGGAAAGGAGTCC  
AAGGGTTACCTGTATTTTTGCCTAGAAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA  
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAAATTTGGAAAAATCTGCCCCAGATACT  
GAACTGGTGAATGTAAACACATCTAAACACAGAGGTAAAAAATTTCTTCAGATACAGGGA  
GTAAAGTTGGATGAGAACTCCGAGAAGCATCTTGTAAAGATTTGAAAGCACAGGGAACA  
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA  
TCAGAAAAGGAGACCCCTCCACCTCTTCCACAAATTGCTTCTCCCCACCCCTTACCA  
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCCTCCAATACAGCTCTT  
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTTAGTCAGGTTCTGCTTCCAGT  
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGCTCTCAGGCAAT  
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA  
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCCCTCCACCCCTTATTACCTGGAGGTGAT  
GACATGGATAGTCCAAAGAACTCTTCTTCAAACCTGTGAAGAAAGAGAAGGAACAG  
AGGACACGTCACTTACTCACAGACCTTCTCTCCCTCCAGAGCTCCCTGGTGGAGATCTG  
TCTCCCCCAGACTCTCCAGAACCAGGCAATCACACCACCTCAGCAACCATATAAAAAG  
AGACCAAAAATTTGTTGCTCGTTATGGAGAAAGAACAAACAGAAAGCGACTGGGGG  
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA  
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA  
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCTGTGAATCAAAATCCTTCGTGAG  
TTAATCCACCGAAGTGTGTTAATGAGGAAATTTGTGAGTATATGGACCATGACTTA  
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA  
ATGGGACTGCTAGAATCTGGTTTGGTGCCTTTTCTGAGGACCATATCAAGTCGTTTATG  
AAACAGCTAATGGAAGGATTGGAATACTGTCAAAAAAGAAATTTCTGCTATCGGGATATT  
AAGTGTCTAACATTTTGTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT  
GCTCGGCTCTATACTCTGAAGAGAGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA  
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG  
AGCTGTGGATGATTCTTGGGGAACCTATTCACAAAGAAGCCTATTTTCAAGCCAATCTG  
GAACTGGCTCAGCTAGAATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG  
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

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## FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTCATTCTTCTGCAGCACTTGATTATTGGACCACATG  
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT  
AAAGATGTGCGAACTCAGCAAAATGGCTCCTCCAGACCTCCCCCACTGGCAGGATTGCCAT  
GAGTTGTGGAGTAAGAAACGGCGACGTCAGCGACAAAGTGGTGTTGTAGTCGAAGAGCCA  
CCTCCATCCAAAACCTTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG  
AACAGCAGCCCGACCACTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT  
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTTATTA  
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC  
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG  
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG  
GAAGCACCCCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCCTGAAGCTTCA  
AGCACACCAGCTGCATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC  
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG  
CCCCGAAGAACTCCCAATGCCACAGGAGGAGGCAGCAGCATGTCTCTCACATTCTT  
CCACCAGAGAAGAGGCCCCCTGAGCCCCCGGACCTCCACCGCCGACCTCCACCCCTT  
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC  
TTGCTGCAACTTTTATCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC  
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC  
ACTGATGGGCCTGAAACAGGGTTTCACTGCCATTGACACTGATGAACGAACTCTGGTCCA  
GCCTTGACAGAATCCTTGGTCCAGACCCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG  
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAGTTTCCAGGGGAC  
CAGGACCTCCGTTTTTCCAGGGTCCCCCTTAGCGTTACACCCGGTGGTCCGGCAACCATT  
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAATTGCAAACTAT  
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG  
GGCCCACTCAGTCTTCTGCTTATGGAAAACCTATCGGGGGCCTACAAGAGTCCCACCA  
AGAGGGGGAAGAGGGAGAGGAGTTTCCTTACTAA

SEQ ID NO: 52\_AA789239\_H

TGAAAATGGAGATGTATGAAACCCTTGAAAAAGTGGGAGAGGGAAGTTACGGAACAGTCA  
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAAGATATTTTATGAGAGAC  
CAGAACAACTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC  
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT  
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTCTATGGACTAGAGA  
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA  
ATAATGTAATCATTCAGAGATATAAAACCTGAGAATATTTTAGTATCCCAGTCAGGAA  
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA  
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAAGATACTTCTT  
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA  
CTGGAAATCCCTATCTTCTAGTAGTTCTGATTTGGATTTACTCCATAAAATTGTTTTGA  
AAGTGNGATTATGCCAGAACTGAAAGCTAAATTAAGTGCAGGAAGCAAAAGTCAATTCAT  
TAATAAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG  
TTTATACCAATACACTGCTAAGTAGTTCACTTTTGGGAAAGGAAATAGAAAAAGAGAAAA  
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAAGTCAAAGGAGGAAGAGGAGATATCTCAG  
AACCAAAAAAGAAAGAGTATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTT  
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTGAACCACCAAAACCTATCAATCCCCA  
GCACTAAGTGAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC  
CCATCAATCTAATAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTACC  
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTACAATCTATTGGAC  
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCTTATCAAAGCCAAATGGAGAAGG  
GTATATTTAATGAGCGAACAGGTCACAGTGACCAATGGCAAATGAGAACAAAAGGAAGC

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## FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC  
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAAATGCTGAAGAGGGAGTCAA  
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC  
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGCTCTATTTTACAAATATTGCT  
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG  
GTTTTTTTTCTGGTAGTGTCTTTCTTTTACATAGTCCAAAAATACAAGATGACAACCTC  
TTCCCGTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC  
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC  
TTTTAAGACTCTGTTGATGTGATAATTTGATTGGAATTATAAAGTCATCTCTCTCTGC  
CTTGAA

SEQ ID NO: 53\_AA124976\_M  
CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT  
GATCTTTTTCGTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG  
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT  
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC  
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC  
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA  
GAGTATGAAGCGACCCAGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG  
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCTCTCAATCCCAGTGAGAATTCTGAC  
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA  
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA  
ACTGAAAGAACAAAAAGAGACGCACTTCTTCACAACTATTGGACAGACTTTGTCTAAT  
AGCAGACAAGAGGACACAGGTCCCACACAAGTCCAAACAGAGAAAGGTGCATTTAATGAG  
CGAACAGGTGAGAATGACCAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA  
TGCGCAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG  
AAAGGGATGGAAGTTAAACAGATAAAAGTGTGAGAGAGAATCAAAGAAAACAGATTCA  
TCTAAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT  
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTCCCGATAGTGCTTT  
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTATTTTATATAC  
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT  
CTATTTTTTTGGTTTTGCTAGCAAAATTTTACAATTTTTCTCTATCTTCCAAAACTGT  
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCTTCTTGC  
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG  
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTCAAGTGGATGC  
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA  
CATTCTATTGTCCCCAGTGAAGCATTATAGTACTTACATAACATGTTACAGTGATATGA  
TGTTCCTAGGTTAACTCCTTGAGATGAACTATTTCTGCACTTCTGACTCCCCCTAGT  
CTAATAGTTCCCTCCATTTAGCCAGAAGAATTTCTGGAAGAAGCGATGCACAACCTGGGA  
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA  
GTTAACAT

SEQ ID NO: 54\_AA575635\_M CCRK\_M  
AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCCGGGTCTTCTCTCCGGAT  
GGTGGTGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG  
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA  
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACCTGTGCTGT  
GTGCTTCGCATCCTGGGTACCCGAGTCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT  
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAAGTGGCCCTGGAGGAGGTGCTGCCT  
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCCTCCTCTACCCTCCACGACAG

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## FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC  
CATCCATCCGAGCTGCCAATTCCTCAGCGCCCAGGGGGACCTGCACCCAAGGCTCACCCA  
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC  
CCAGAACTGATTCCGGCCCTTCATCCCAGAGGGGTGAGATG<sup>et</sup>TGGTCCAGGCCTTCCTGCT  
CGCCCTAGGAGCACCTCTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA  
CACCTGGTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA  
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA  
GCTGTGTCCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC  
AGGCTCTGTCCCCCTCTTCAAGGACATTGGTACTACAGCACCACTGGTGGAAGCACAGAG  
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT  
CCACTGGGTGAGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTTCTGTCTAATTGCACC  
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTCACAGGGGTGAGGTA  
CAGAAGGGGCCCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTCACGGGA  
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG  
TTCCCGAAGCCCACTTCCCACATGTCGGGTGGGTGAGTCACTGAGCCTGAGGCTGCCTTG  
CAGATGCGGAAGCAGGCATTCCTGGAATCCACTCAGTAAATAAATTCAGTGTGACTCAG

SEQ ID NO: 55\_AA631990\_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA  
TCTGGTCACTCACTATCCATTCATGATTACAACCTCTTCAATACTATCGCGGCCGAGGA  
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG  
CGGCATTCAAAAGAACTCACTGTCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA  
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG  
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCAATTATTTAGAAGCAAGGTC  
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT  
GAAGGATATGTTCCCTAGACATTATCACAGAGACATTGAAAGCGGGTATCGAATCCACTGC  
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCATAAAGGAAGCGCAATAGACACTGT  
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGACCTTTGGC  
AAAGTTGTAGAGTGCAATTGATCATGGCATGGATGGCATGCATGTAGCATGAAAATCGTA  
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTTCAGAAATCCAAGTATTAGAGCACTTA  
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT  
CATGGTCATGTTTGTATTGTGTTTGAACACTGGGACTTAGTACTTACGATTTTCAATAA  
GAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC  
CAGTCAATAAAATTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT  
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTTCTAAATGAAACGTGATGAA  
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT  
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCAATTTGGCT  
TTAGGTTGGTCTCAGCCTTGTGATGTTGGAGCATAGGTTGCATTCTTATTGAATATTAC  
CTTGGTTTTCAGTCTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA  
ATATTAGGACCCATACCACAACATGATTAGAAAACAAGAAAACGCAAGTATTTTTCAC  
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC  
AAACCGTTGAAGGAATTTATGCTTTGTGATGATGAAGAATGAGAACTGTTTGACCTG  
GTTGGAAGAATGTTAGAATATGATCCAACTCAAAGAATTACCTTGGATGAAGCATTGCGAG  
CATCCTTTCTTGACTTATTAATAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA  
CTTCTCTAGAAGAGATTACTTAAGACTGTGTGAGTCACTAAACATTCTAATATTTTTGT  
AAACATTAAATTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT  
AATTAAGTGTAAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAATTTT  
TCTTTTGAATTAACATTTTAAATAACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT  
GTGATTGATCTTGCTTTTGTACATGGAGGTCACTCTGAAGTGATTTTTTTTGTAGTAAA  
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

FIGURE 2SS

ACTTAACTTTAAAAGTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAACCTCTAG  
ATAAGCAGGTACTAGAAACCAAACCTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT  
TTAAGTGTGTATTCTTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA  
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAAACCATACACACTTTATTT  
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT  
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC  
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAAATACGTAAACCTAT  
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG  
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAAATTAATTGA  
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56\_AA557536\_H

AGTAAGGCCCCGCGGGCGTCTGGCCGCCATGTGCAACCGTAGTGACCCTCGCATTGTCC  
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC  
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA  
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCCTCGGCCTTCCAGCC  
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACC  
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC  
TGAACGCAGTCATCCGGAAGGGCGGCCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT  
ACCAGTCCCTGCGGGCCACCCGGTTCTCCTCACTCGGGGCACGTTGTGCACCGGGACCAGA  
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG  
CCCGCTCCCTGGGCGACCTCCCTGAGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG  
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTCGCACCGCTACACCGCTTCTCT  
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC  
TGCGGGGGGAGACCCCTGTTCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG  
AGACCATCCCAACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC  
CGCCAGACACCTCCCCAGAGGCCTTGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG  
ACAAGCGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCACTGCC  
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGGCCCCGGGCACACGAAGGGGTCCAGC  
TCTCTGTGCTGAGTACCGCAGCCCGTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA  
GCGGCACCTCGAGAGAGAAGGGCCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA  
AACCCAGAGCCGACCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC  
CCCAGAGCAGCCAGGCCATGACCCTGCCAGCACGAGTCCCCCGTGCAGCCAAGAACG  
TTCACAGGCAGAACTCCGCTCCCCTGCTCCAAACTGCTCTCCTAGGGAATGGGGAAAGGC  
CCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG  
GAGCTGCGCCCTCCCTGACCTCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC  
GGGTGACTGGAACCGGGGCGGTGGGGTGAAGGTGGCCAGCGTACAACAGGTCCCTCCCC  
GGCTTCCCTCCGAGGCCCCGGCCCCGGGAGGATGTTTCAACACCTCTGCCTTGAGGGTG  
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC  
ACTCGGCACTGGGCCACCTGCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC  
CTTCACTGGCCCTCTGTTCCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG  
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCCGTGAAGTTCCAGGGAGCTTGCCCCGGGT  
CTCCTCGGGGGAGCAGATGAGGGCCCTGCC

SEQ ID NO: 57\_N28606\_H, MOK\_H

ATGAAGAACTATAAAGCAATTGGCAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG  
ATGCAAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAA  
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC  
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGACTA  
ATATGTGAACCTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATACCCATTA



## FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTAC  
AGAAATGGAATATTTACAGAGATGTAAACCAGAAAAATACTAATAAAGCAGGATGTC  
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA  
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTTCTACACG  
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTCTTCTACGAGATCGCCAGTCTGCAGCCC  
CTCTTTTCTGGAGTAAATGAACTGGACCAATCTCAAAAATCCACGATGTCTATCGGCACA  
CCCGCTCAGAAGATCCTCACCAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCCT  
TTTAAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC  
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG  
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA  
AAAGCTGGCTTTCCGGAGCACCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT  
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA  
CGAGGACCGGCCTATGTCTGGAAGTGCCTAAAGCTTTCCGGAGTGGTCAGACTG  
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG  
CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC  
CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58\_AB023153\_H, ICK\_H  
ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCTCTGCTG  
GGAAGAAGCATTGAGTCTGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT  
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC  
AATGTAGTCAAATTAAAAGAAGTTATCAGGGAATATGATCATCTTTATTTATCTTCGAG  
TACATGAAGGAAATCTTTACCAGCTCATTAAAGAGAGAAATAAGTTGTTTCTGAGTCT  
GCTATAAGGAAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAACTCGGC  
TTCTTTTATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA  
ATTGCAGACTTTGGTTTGGCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA  
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCCC  
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTTACACCCTCAGGCCACTCTTC  
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTGCTGGGGACACCAAA  
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCAATGAACCTTCGTTGGCCACAG  
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC  
CTGAGAGACATGCTTCAGTGGGATCCCAAGAAACGACCAACAGCTAGTCAGGCACTTCGA  
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCACACAAACCTTCAGGATTCA  
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC  
CCACCTGCCCAGCCACCAGCCAAGCCACACACACGAATTTCTTCACGACAGCATCAAGCC  
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC  
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCCGTGCTTTTCCCATCCCTCCACAACAAG  
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAAATGGTGAGATAAAGCCAAAG  
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC  
TTGGATGACTTGATTTTCACTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA  
CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTGTTTGGACCTGAAGCCCTCTGAGCCT  
GTGGGCACAGGAAACAGTGCCCCCAGACGTCATATCAGCGGCGAGACACGCCACCT  
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTTGCTGGGATCAGT  
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT  
AGTTCTGGCTTGTCTGGAATCTTTCAGGGACAATGTGAGTAATCAGCAAAGTAAATTC  
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG  
AAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTTAGCACCTATTCCAGACCCTTCC  
CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATCTTGGACACC  
CAGCCTAGAAGCACTCCTGGGTTGATACACGGCCTCCAGCCGCCAGCCAGTGCATGGC  
CGGACAGACTGGGCTTCCAAGTACCCATCCCGCGGTGA

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FIGURE 2UU

SEQ ID NO: 59\_AA839940\_M  
AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG  
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG  
CAGCAAGGCATAGACCCAGGAGCAGTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT  
GGCCAGGAAGAAGCTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT  
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTTGAACACCGGGTAGTGAGCATCAAAGAT  
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTTCGGTTT  
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC  
AAAGTGAAGAACGTAAAGGACCGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG  
CTCAGCCACGTAAACTTGATCCAACCTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT  
CTGATCATGGAGTATGTGGATGGAGGCGAAGCTTTGACCGGATCACGGATGAGAAGTAC  
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC  
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTGCAGC  
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATACAAGCCTCGG  
GAGAAGCTAAAGGTGAACCTTGGTACTCCGGAGTTCTTGGCCCCAGAAGTTGTTAACTAT  
GAGTTTGTGTCATTTCACACAGACATGTGGAGTGTGGGAGTTATCACTACATGCTACTC  
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC  
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTGCGAGGAAGCCAAGACTTT  
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTCCCTGAAA  
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAAGTTCGCCTCAGATCC  
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG  
GCTGCAGTCAACAGGCTACGGAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC  
CACTGGGCCTGGGAATTTCTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA  
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTATTTTGCAAAGAATGATGGA  
AGGAAGCAAGAAAGAAAGAAAGAAAGAAAGGGGGAAGAAAGGAAAGGCAAGCAAGCAA  
GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTGTTTTATTAAAGCCCTAG  
GAATGTTTTTCTGCCTCGTAAGGTGAGGCTCTCATATGCTGCTTACCCCGCACCC  
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT  
TGGTCAAATTTGAATTTCTAACTTGTGATGATTAAAGAAGCCAGTAGGGAGGGATG  
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA  
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60\_AA460132\_H  
GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG  
TGTCCGGGGTGGACGATTTCGGGTAGCCGAAGAAGTCCCAGGATTGCCGAAGAAGTCCCA  
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTGGAG  
CTGTTGCGCGGAGCAGTCATGGCGGCGCCAGAGCTACTACGCGGCGGATGGCGAGGAG  
CCCGCCCCGAGGCTGAGGCTCTGGCCGCGAGCCCGGAGCGGAGCAGCCGCTTCTTGAGC  
GGCCTGGAGCTGGTGAAGCAGGGTGGCGAGGCGCGCGTGTTCGCTGGCGCTTCCAGGGC  
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG  
CGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCCGGCGCTCCTCCGCTGTGCGCGCGCT  
GGAATATCTGCCCCAGTTGTCTTTTTTGTGACTATGCTTCCAAGTCTTATATATGGAA  
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA  
ACTCCCCAGGGTCTCTCCAACCTAGCCAAGACAATTGGGCAGGTTTTGGCTCGAATGCAC  
GATGAAGACCTCATTGATGCTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG  
GAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTCAATTCAGCACTTCCAGAG  
GATAAGGGAGTAGACCTCTATGCTCTGGAGAAGGCCTTCTCAGTACCCATCCCAACACT  
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAAAGGCCAGGCCA  
GTGCTAAAAAAATTAGATGAAGTGGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG  
AAGAATGTGTATGACAACCACACAGTGAAGCTCTTTTTTCAAAGTAAATTTGAAGAA

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## FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTAAAGTGGTATGTG  
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT  
AGGCAGAAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCAGATTGTGACATGTA  
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTAG  
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT  
AACCCAGTGTTTTTTTTGTGTTGTTGTTGTGTACATGTTATATTTATTTTGAACCAGTTT  
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61\_SGK034\_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG  
GACACGGAGGAGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC  
TTCCGGCGGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGCTGGTGACCAC  
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC  
ATCTTCATCACAGAGTACGTGTCTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG  
AAGAACCACAAGGCCATGAACGCCCCGGGCTGGAAGCGCTGGTGACGACGATCCTGTCT  
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC  
ACCATCTTCATTAGCACAACGGCCTCATCAAGATCGGCTCCGTGTGGCACCGAATCTTC  
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACCTCGG  
AACCTGCACCTTCTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC  
TTCTCTTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC  
ACCCGGGTACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG  
CGGGAGTTCATCCTTTGCTGCCTGGCCCCGGGACCCCTGCCCGCCGGCCCTCTGCCACAGC  
CTCCTCTTCCACCGCGTGCTCTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC  
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG  
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCCGCAGGCCCCCGCTGCAGTGGCGG  
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTGAGGAATGGAATC  
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCGCTGTGCTGGCCCCA  
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC  
AGAAAGGTTCATCCAGATGCAGTGCAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT  
CTCACTCTGCTTCTGGTGTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC  
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACTATGGCTTCCTCCACGAG  
GACGACCGGATGAAGCTGGCCGCTTCTGGAGAGCACCTTCCTCAAGTACCGTGGGACC  
CAGGCCTGACCCGGAGCCCCAGCCCCAGGACCATGCCGGGGTGTGCTGCCCGGGCAGGCC  
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAG  
GCCCCGGTAGTGAAGGAACCCCCGTCTCCTGAGAGTGGGGCTGACCCTGCCTTGGGCGC  
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCAGGTCTTAGGATCAGG  
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCTTACCCAGGCT  
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCAGC  
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCAGGGAACCTGCTCCAT  
GGGGTCTGGGAGAGCAGCCATCCCCTGCTGGCACCATAGACCCACACAAGGAGCCTGCAC  
AGCAAGCCAGCGGTGACACACCTGCAGGTGTGAGGCATGGCACTGGGCACAACAGGGACC  
TGGCAGGAGAAAAGACACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAAAGCCCTT  
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCCTGAGACCAG  
AAGTTGAGCCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCCTCAATGGGCTTTTTC  
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC  
TCACAGCCCCCTCCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCCTGGGCCCT  
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA  
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT  
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA  
CATTAGCGCATTTCATGCCTTTCTAAACGCATTTCAATGTCAACCAGGAAGGCACACCAC



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## FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT  
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA  
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCTTCTCAGGGTCTATAGATGAAC  
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGGAGAACAGCCGTG  
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA  
AATAAACAGATTTGTCATGGGACATCTAATAAATTAAATGAACTCTG

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CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGCGCCGCGAG  
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCTCTCGCCGCGGGCTCCTGCCCCCAAGA  
ACGGCTCCAGCTCCGATTCCTCCGTGGGGGAGAACTGGGAGCCGCGGCCGCGGACGCTG  
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCACACTATGGACAAGGACAGCCGTG  
GGGCGGCGCGACCACTACCACCACTGAGCAGCCTTCTTCCGCGGAGCGTCTCTGCG  
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCTTCTCTTCCCTGCCCCAGCCAGCA  
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG  
CCACCGCCACTTCCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCCCTGGGGAACAGG  
CCGTCGCGGGGCCCTGCCCCCTCGACTGTCCCCAGCAGTACCAGCAAAGACCGCCAGTGT  
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGGAGCCGCCGCGCGGAGAAAGTGGCAGCGGCG  
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC  
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTCTCAAGTTTGACATCGAAA  
TCGCCTGGTGTGAACTGCAGGATCGAAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG  
AAGAAGCTGAAATGTTAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT  
GGGAATCCACAGTAAAAGGAAAGAAGTGCAATTGTTTTGGTGACTGAACTTATGACGTCTG  
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT  
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC  
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG  
GAGACCTCGGTCTGGCAACCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC  
CAGAGTTTATGGCCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG  
CTTTTGGGATGTGCATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA  
ATGCTGCGCAGATCTACCGTCGCGTGACCAGTGCGGTGAAGCCAGCCAGTTTGTGACAAAG  
TAGCAATTCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA  
GATATTCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG  
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG  
AAGATATTAAGAAATTAAGGGAAAAATACAAAGATAATGAAGCTATTGAGTTTGTGTTTG  
ATTTAGAGAGAGATGTCCCAGAAGATGTGACACAAGAAATGGTAGAGTCTGGGTATGTCT  
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA  
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAAAAGCAGGAAGAGA  
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC  
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCACTTCACTTCTACACAAG  
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACACTACAGTACCAGCAACCCAGTA  
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAAGGATCCTCTGTCTTACAGAAT  
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCCAANNCATGAACAGGCACATT  
CTACAGGCACAGTCCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG  
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCTCCTCAACAGA  
CAGTGACAGTATTCATTTACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG  
TGAGTCAAGCCTCAAGCTCCACAAGTCTTGCCTCAAGTATCAGCTGGAAAACAGAGTACTC  
AGGGAGTCTCTCAGGTTGCTCCTGACAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC  
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGATGTTGCTTCAAGGTATGA  
GTGATGGCAATGAGAACGTCCCCTCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

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## FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAAT  
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC  
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG  
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGTGGTTTGTGGATC  
AAGTGCGAGAAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTCAGTGTGGAAC  
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTCAGGTT  
CTCAGAAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA  
TAGGCATTCTACAGTTCTTTAACTCAAGTTGTTTCTGCGGGAAGGCGGTTTATAG  
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAAAGTTTCCCCAGTGAAATAACAG  
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT  
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA  
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT  
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA  
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG  
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCCA  
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG  
CAGTTGTCTCAATATCTACTACATCCCCGTCACCTCAAGTCCCCACATCCACATCTGAGA  
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG  
CAGGGGGCAGTACTGCTACCCCAAGTCCCTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG  
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA  
GCACAGCTTCACAGCTGTCCATTACAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG  
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT  
TGGCTTTCTCCCTCTCTGCACCATCTTCCTCTTCTCCTGAGCAGGAGTGTCTAGTT  
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTTCATTCCATCAGTGATAGCTTCTACTC  
CTATTCTTCCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA  
TCCCACCCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA  
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCTGAGTAGATT  
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC  
GGTCTCTGTTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA  
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCAACTACTGCTGTTGCACCAA  
GCAAACCTCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCCTAGGAA  
CAGTTGCTTTGCCAGTTACACCAGTGGTTCACACCTGGGCAAGTTTCTACCCAGTCAGCA  
CTACTACATCAGGAGTGAAACCTGGAAGTGTCTCCCTCCAAGCCACCTCTAATAAGGCTC  
CGGTGCTGCCAGTGGGTACTGAACTTCCAGCAGGTACTCTACCAGCGAGCAGCTGCCAC  
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT  
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGAATCTGCGGTTGGTCTGTGTCCA  
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTCTCAAG  
TCAAAGAAGGCCCTGTCTAGCAACTAGTTCAGGAGCTGGTGTCTTTAAGATGGGACGAT  
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG  
CAAAGTCTGTTCAATTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC  
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG  
ATGTGCCAGAGAGTGCCCAAAAATACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC  
CTACCAAGGTTGGACGTTTTTCAGGTGACAACTACAGCAAAACAAGTGGGTCTGTTCTCTG  
TATCAAAAATACTGAGGACAAGATCACTGACACAAAGAAGAAGGACCAGTGGCATCTCCTC  
CTTTTATGGATTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG  
AACTGTGAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGGAGGCCGCTTTTTTAA  
GTAGGGATGTGGATGATGGTTCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA  
GCCTTCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCTGCTTACATGA  
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC  
GAGATAAACATCTCAAAGAGATTCAGGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

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## FIGURE 2ZZ

CTTTGTATACCAAAGTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC  
TTTCAGGGAGAGAAGACGACGACCCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT  
CCTTGGGGGAATAAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG  
TCTTGCACCCCCCAGCAGACCCTCCACCCTCCTGGCAATATCCCAGAGTCCGGGCAGAAATC  
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTACGCCTTCACCA  
GTGATGGTGCCATTTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA  
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG  
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACTGAAGAATCTGG  
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA  
ATTACTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC  
TCATTTGGGATTTGGAACCTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAATTCT  
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA  
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA  
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATCCCACAGAG  
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTGGGCATCTGGGTGAGAA  
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA  
GATCAGTCTCTTCACAGGAAGAATGCACCTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT  
TATTCGAACTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT  
CATCTCTTACATATCTGACCTTCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG  
CATTTACCACTCCAGCCTCAAGTTTCTAACATCTTGTAGTTGTGTTCTGTCTCTTCTCC  
TCTCTCTGTTCTACCTGTTTTTCCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC  
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTTCTGAGTACGCCCTGCTT  
GGCTCTTTGTGTGTAAACACCTTTACTCCTTCTTGTCTTGTGTTTCTGCTGCTTGGATC  
TGATGTTTCACGCAGTCCATTTTCATTTGTCTCTTTTGTATATCATCTACTCAGTGGCT  
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACAATTAATTATGATAAAAAATG  
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACCTTCTGGTAGAAGTGCTTCTTCAT  
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTTAGAAT  
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT  
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA  
GGCGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC  
CCATCTCT

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GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT  
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCTTCCAGCATGTCGGA  
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC  
AGCTCCTGGCCTGACATCAGTGTACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC  
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGGAAAGAGTCGCCCTGTGGGCG  
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA  
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA  
ACGCAAGAACTACAAGCTGCAGGAGGAAAAGGTTCTGTCTGTGTTTGATAATCTGATTCA  
ATTGGAGCATCTTAACATTGTTAAGTTTCACAAATATTGGGCTGACATTAAAGAGAACAA  
GGCCAGGGTCATTTTTATCACAGAATACATGTCATCTGGGAGTCTGAAGCAATTTCTGAA  
GAAGACAAAAGAACCAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGACACACA  
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT  
GACCTGTGACACCATCTTCATCCAGCACAACGGACTCATCAAGATTGGCTCTGTGGCTCC  
TGACACTATCAACAATCATGTGAAGACTTGTGCGAGAAGAGCAGAAGAATCTACACTTCTT  
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG  
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAATGGAGAGTCCTCATATGT  
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

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## FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT  
CCACCCAGCATTGTTTGAAGTGCCCTCGCTCAAACCTCCTTGCGGCCCACTGCATTGTGGG  
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAAACATGGATACTAG  
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTCAGACTTTGTACTC  
TCAGTCACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC  
TCTGACAGCCTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC  
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA  
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGGAGTCAAACACCACCTGAC  
ACTTCTGCTGAAGTTGGAGGACAAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA  
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA  
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA  
CAGTACCCCTCAACTCAGCCGCTGTCAACGTCTCCTCTTAGAGCTCACTCGGGCCAGGCCC  
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC  
AGTATTACCCTGTGAAGCCCCCTTCCCTCCTTTATTATTACAGGAGGGCTGGGGGGGCTCCC  
TGGTTCTGAGCATCATCCTTTCCCTTCCCTCTCTTCCCTCCCTCTGCACTTTGTTTACT  
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGCTAGT  
CGCTGATCTGCCGGCTCCCGCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA  
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGAGAGAAAGGTGGTGCTGCAGTG  
GTGGCCCTGGGGGGCCATTGATTGCCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT  
GCT

SEQ ID NO: 65\_AA711829\_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG  
AAACGCTGGTGTACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCC  
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG  
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAACAG  
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCACAAACGTGACAACAGCAGTG  
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTGAGGGCAAT  
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC  
TCATTACAGAGGGAGTTTATTCAAAGTGCCTGCAGTCTGAGCCTGCTCGGAGACCAACA  
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCTCACTCAAGCTTCTTGCT  
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC  
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA  
GTTGAGACTTTGTACTCTCAGTCACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC  
AGGAATGGGATCTACCCCTTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG  
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT  
GAAGTGGAGACACGAAAGGTGGTGCTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA  
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC  
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC  
TTCATTAGTGAGGCTGATCAGAGCCGCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG  
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTACCGTCTCCTCGTAGAGC  
TCACTTGAGCCAGGCCCTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCACTCCTCCT  
GTCCCTTCTCCCCAGTCAGTATTACCCTTCGCGCCCATATTATTAGGAGGGCTTTAGGG  
GCTCCCTGGTTGAGTATCACCTGCCCTTCCCTCTCTTCCCTCCCTCTGCACTTTGTT  
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC  
TAGTAGCTGACCTGCTGCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG  
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA  
GGGGTGGCCCCCGGGGGGGCATTGGAATCACCTCAGTTGCTGCTGTAATAAAGTCTAC  
TTTTTGCT

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## FIGURE 2BBB

SEQ ID NO: 66\_AA099102\_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG  
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCTC  
TCATCCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTTCACCGAGTGTGAGCCG  
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG  
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCCCACCTCTCCGGTCGCAAGCTGTCT  
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC  
TGCATCTGCCCCGTCCCTGCCCTACTCACCCTGTCAGCTCCCCGCAGTCCTCGCCTCGGCTG  
CCCCGGCGGCCGACAGTGGAGTCTCACCACGTCTCCATCACGGGTATGCAGGACTGTGTG  
CAGCTGAATCAGTATACCTGAAGGATGAAATTGAAAGGGCTCCTATGGTGTCTGTCGAAG  
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAAG  
CTGATCCGGCAGGCCGCTTTTCCACGTGCGCCTCCACCCCGAGGCACCCGGCCAGCTCCT  
GGAGGCTGCATCCAGCCCAGGGGCCCATTTAGCAGGTGTACCAGGAAATTGCCATCCTC  
AAGAAGCTGGACCACCCCAATGTGGTGAAGCTGGTGGAGGTCTTGGATGACCCCAATGAG  
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC  
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC  
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC  
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT  
GACGCGCTCCTCTCCAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT  
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA  
TACTGCTTTGTCTTTGGCCAGTGCCATTTCATGGACGAGCGGATCATGTGTTTACACAGT  
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG  
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGGCCGAAATC  
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTGCGAGGATGAGAAC  
TGCACGCTGGTTCGAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC  
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATT  
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTGAGCGCCTGGAACTTGCTCACCAAAAAA  
CCAAGCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT  
CCAGGGCACCGACCCGCCCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC  
TGCGTGGAAAGTTGCTGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG  
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67\_5R69\_17\_2\_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTGCGAGGGGGAAGTGTGCGAGC  
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGCACTGGACAGAAACA  
GCCATCCAAGTGGCTGAGTGGAGGGACCCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT  
CCCTCAGGTAGGGATCGGGGCGCCTTGTCGCGCCAGCCACGTGTGGCGTCCGGTACAGT  
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC  
GCGTTTGGAACTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA  
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA  
TGGAATAATTGAAGCATATTATCACCTTGGCCAGGTTCATCCACAAACGGTGTGAAGAGA  
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCTCGGCCTGATCAAGC  
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG  
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTACAGCA  
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG  
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAGGTTGAGCAAC  
GCATGCCTGTTTTACCCATAAGCCAAGGAGCGTCTGGGCACAGGAAGATCAGCAGGATG  
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAATAGAAGCTT  
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAAACTTTGAGGCAGTGTAAGT  
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAAGTAGAAGTCATCAGTTTACTGGGAC

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## FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC  
CACAGGTTTGGGGATCCATTTCATGGCTAGCCAGGCTTCTGTCCATGGAATAACATGTGG  
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT  
ATGAATAGAATCAAAGCTTCAGTTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAA  
TTTAAATGCCCCTCATTTCATTTCATCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA  
GGCCATGCAAAGAGGTAAGTGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG  
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG  
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC  
CAAGCTCTGGGTAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG  
GGTTAAGGCTGGAGGGACAGGCGGGATTTGAAGAGGAGGGAAAGGAAGTGGATGACACAT  
TCTGTCTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT  
GGGCTGAGTCCATCAGAAGCCCCAGCCACCAGCTCTGGTTCATGTAGTAGAGCTTCC  
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGCTCATTGACTCT  
TTTGTCTTCTTTCCTCTCGGGGGTGAGGTTCAGATTTACCACCAAATATGCAGGAGAT  
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT  
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC  
CATAAAGTATTCAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA  
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT  
TTGCATTGATGAAACAGTGACTCCGCTCAATTCTCCATTGTGATGGAGTACTGTGAAGT  
CGGGACCTGAGGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGCGAAGCGCATGGT  
CCTAGTCTGGGGCAGCCCGAGGCTTATACCGGCTACACCATTGAGAAGCACCTGAACT  
CCACGGAAAAATCAGAAGCTCAAACCTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC  
AGGATTTGAGTTGAGGAAAACACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC  
AGACAGAGTCAAATCTACAGCATATCTCTACCTCAGGAACTGGAAGATGTATTTTATCA  
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCTCTGGGAAATCGCCACTGG  
AGATATCCCGTTTCAAGGTGAAGAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG  
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC  
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCATGATCCCTCTGTGCGGCCCT  
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA  
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAAGTGGACATCTCTCTCTCAT  
ATCCTTCGGCATTTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTTACAAAT  
AGAAAACGATTCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA  
CCTCTGACAGTAACCTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT  
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATTT  
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGAAGTGTAT  
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC  
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT  
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA  
TCAAGACCAGAAGAACCACTCAAGCAGATCCCAGCCCAAATTGCCCATTCACACAATCAG  
GAGCTAAATAAATTACTGTTGTCTTTT

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CGCCCCGGCCCCCTCCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT  
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCCGACTGAGGCTGGGGG  
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCGTTGCCATGAACCGCGGACACCCCGGCC  
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCTCACACCC  
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGGG  
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT  
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCCAAGCCTACCTT  
ACGAGCAGACCATCGTCTTCCAGGAAGCACCGGGCACATCGTGGTCACCTCAGCAAGCA

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## FIGURE 2DDD

GCACCTTCTGTCAACGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTCGAAGCACTG  
TGAGCCTCCTTGATACCTACCAAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA  
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG  
GGGCCACTGTGCGCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA  
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG  
AGGTCTTAGAGTTCTTGGGCGGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAACGGG  
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCCGACAAG  
GTCAGATTGAAGTGAGCATCCTGGCCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT  
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT  
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT  
ACATTCGCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAACTCAAAGCCTAGGTC  
TTATCCACGCTGACCTCAAACCAGAGAAATCATGCTGGTGGATCCATCTAGACAACCAT  
ACAGAGTCAAGGTCACTGACTTTGGTTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA  
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG  
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCGAATTGTTTCTGGGTTGGCCGT  
TATATCCAGGAGATTCCGAGTATGATCAGATTCCGTATATTTCAAAAACAGGGTTTGC  
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG  
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA  
TTAAGTCAAAAGAAGCAAGAAAGTACATTTCAACTGTTTAGATGATATGGCCCAGGTGA  
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT  
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG  
AAACCCTGAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC  
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA  
CGGTGAACCAGAGCAAAACCCCTTTCATCACGCACGTGGCCCCCAGCACGTCCACCAACC  
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA  
TGGCTGCAGTGGCCCCAGCGAGCATGCCCCCTGCAGACAGGAACAGCCCAGATTTGTGCC  
GGCCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG  
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAAATGCAGTTCCCATCGTCA  
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCAGCAGGCTT  
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG  
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC  
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC  
AGCCTGCACCTATTGACCGGTGATGTGACCCCTCCAGCAGCACAGCCCTTAAATGTGGGTG  
TGGCCCAGTGATGCGGCAGCAGCCAACCAGCACCACTCCTCCCGGAAGAGTAAGCAGC  
ACCACTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT  
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACAACCTCCCCGCTGTGCCATGGTGCACA  
GTAGCCCCGGCCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACCA  
CCCCGGAACGGCAGCGGCAGACAATTGTCAATCCCCGACACTCCCAGCCCCACGGTCAGCG  
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA  
CTGTCTCCAAGCAAAGAAAAACGTGATCAGCTGTGTACAGTCCACGACTCCCCCTACT  
CCGACTCCTCCAGCAACACCAGCCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG  
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA  
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG  
TGCCAGTCAACACCAGTCAACCACTCGTCTCTACAAGTCCAAGTCTCAGCAACGTGA  
CCTCCACCAGCGGTCACTCTTCAAGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC  
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA  
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCACCATGG  
CCCAGGCTCCGTACTCCTTCCCCGACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC  
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG  
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCCCACCTGGTGGCCTCGCAAGGCTCTG

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## FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA  
GCATGGGCCCCCGGTCTGCCCCTCGCCCACCATCCACCCGAGTCAGTATCCAGCCCAAT  
TTGCCACACAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCAC  
TGAGCCCCGCCAAGGTCAACCAGTACCCCTTACATATAAACACTGGAGGGGAGGGAGGGAG  
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGGAGGGAGAGAAGGAGGGAGGGCGCTCCTGGGA  
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG  
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAAGTGAACTTGAACC  
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTTTAAAGGAAGGATTAAAGAG  
GGTGGGAAATCTATGGTTTTTTATTTTAAAAAAG

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CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTTCGAGAGTACCCGTGGGAGCGTCGCG  
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCGACCCCCAACTGGCGCCT  
CTCCCCGAGCGGGGTCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA  
GGATGCGGGGCGCCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTG  
TATGACACCTTCATGATGATAGATGAAACCAAATGTCCCCCTGTTCAAATGTACTCTGC  
AATCCTTCTGAACACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA  
GATCATACTCAGCACTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA  
TTTGGCAACAGAAAATCCAATACTATTTCAGTCAGATGGCATCAGTGAAGTCTGAAAAATGC  
TCTCCTACTGTTTCTCAGGGTAAAAGTTTCAGATTGCTTGAATACAGTAAAATCCAACAGT  
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA  
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTA  
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT  
GATGCAGATGGGGCCTATATTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG  
CTGAAAATTATTGGCAAGGGGAGTTTTGGGCAGGTGGCCAGGGTCTATGATCACAACCTT  
CGACAGTACGTGGCCCTAAAAATGGTGCCTCAATGAGAAGCGCTTTCATCGTCAAGCAGCT  
GAGGAGATCCGGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT  
ATCCACATGCTGGAAAGTTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG  
AGCATAGACCTTTATGAGCTGATTAATAAAAAAATAAGTTTCAGGGTTTTAGCGTCCAGTTG  
GTACGCAAGTTTGGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT  
ATTCACTGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC  
AAGGTCAATTGACTTTGGGTCCAGCTGTTTTCAGTACCAGAAGCTCTACACATATATCCAG  
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC  
ATATGGAGTTTTCGCTGCATCCTTGCAAGCTTTTAACAGGACAGCCTCTCTCCCTGGA  
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA  
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATAACCCGCTAC  
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTCTGCTCACGTAGG  
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT  
GACTACTTGTATTATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG  
ACCCAGCTCAAGCATTAAAGACACCTTGGATTAGCAAGTCTGTCCCCAGACCTCTCACC  
ACCATAGACAAGGTGTGAGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCAGGGATTG  
GGTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA  
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA  
GAGATATGCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAATGGA  
AAAAATGCAAGCCCATTTGGTGGATGTTTTTGTGTAGAGTAGACTTTTTTTTAAACAAGACAA  
AACATTTTTATATGATTATAAAGAATTCTTCAAGGGCTAATTACCTAACCAAGCTTGTAT  
TGGCCATCTGGAATATGCATTAAATGACTTTTTATAGGTCA

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## FIGURE 2FFF

SEQ ID NO: 70\_AA589241\_M DYRK3\_M  
CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG  
CCAAGTACTTTTATTAACCTCAAAGGCTTGCCCTCGATACTGCTCCGTATCTACCCAGACGG  
ACGGGAGGGTGGTGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCGCCAG  
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTTCATAGAGTTTC  
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCCGCTCACCCCGGCTCAAGCATTAAGAC  
ATCCTTGGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC  
GGGTAGTTAAACCTACAAATGCTTTCCAGGGACTGGGTCCAAGCTGCCTCCAGTCTGTTG  
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT  
GCAGTGTATTGCCAAAGCTGATTAGCTAGTAGGACCTCAGAGACTGATACATATCATAT  
GTATTTTAAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC  
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTTATATGACTAT  
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT  
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71\_5R72\_16\_2\_H  
GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA  
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA  
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA  
AATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA  
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCTGAAATAGAGTTAAAAAA  
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAATCTCGCCTAGAAGAACTGGC  
CAAGAAACACTGTGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT  
CAGCGAGCATAACAAGCCCCCTCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC  
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA  
AATCCTGCATGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA  
AATGGCTAAGCAGGAACGTTTGGAAATGCTAGTTTGTCAAACCAAGATCATACCTCTAA  
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT  
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAAGCAGTATTCT  
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATCTGTATTTCAATATGGGGAG  
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGTATGAACAACCTGGAAA  
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTGTATGAGTGGGT  
CCTTCAGTGGCAGAAAAAATGGGTCCATTCTTACCAGTCAAGAAAAAGAGAAGATTGA  
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAATTTAG  
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT  
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC  
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTGAGCCCTTGA  
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCTGAGTGCATCTAATGTCTTGGTGGA  
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG  
CAAGGAGGATGTGTTTGGAGCAAACCCGAGTTCTGTTTGTGACAATGCTCTGCCTTATAA  
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG  
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGAATTTCTAAGCGCCTCGCAGACATTTG  
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT  
GAAACACAGCTTTATAAATCCCCAGCCAAAATGCCTCTAGTGGAAACAAAGTCTGAAGA  
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC  
CTTCTTTAGTGAGACACAGAGACAGTTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA  
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCTCAAGGTGCAGAACAAAGTTGGACGGCTG  
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA  
GGGCGAAGTGACACTGCTGTACAGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC  
CTGGATCGAGCGGCACGAGCGGCCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

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## FIGURE 2HHH

TCATCATAATTTAAATTAATTTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA  
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAG  
CCT

SEQ ID NO: 73\_R43524\_H, HRI\_H  
ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT  
GTGGCTGCGCCGCGGCCATCGACTTTCCCGCCGAGGGCCCGACCCCGAATATGACGAA  
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAAGAACCCCTACAACAGCCAACTTCCCT  
TTTGCACTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT  
GAACCAAACCCACTTCGTTCAAGACAGGTGTTAAGCTACTTTGCCAGACGTTTATCAAA  
ATGGGGCTGTTGTCTTCTTTCACTTGTAGTGACGAGTTTAGCTCATTGAGACTACATCAC  
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTTCGTCAGGATCCTTGT  
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGGAAGCACAACCT  
TCACGTTACTTAAATGAATTTGAAGAACTTGTCTATCTTAGGAAAAGGTGGATACGGAAGA  
GTATACAAGGTGAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT  
AAGGGTGCAACTAAAACAGTTTGCATGAAGGTCCTACGGGAAGTGAAGGTGCTGGCAGGT  
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCTGGATAGAACATGTTTATGTGATT  
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG  
GAAGAGGACAGAGAGCAATGTGGTGTAAAAATGATGAAAGTAGCAGCTCATCCATTATC  
TTTGCTGAGCCCAACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAAATCAG  
AATAACAAGTCCGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG  
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA  
CAGCAGCTGCCACTCAGGCGTAATCCACCTAGAGGAGAGTTTACATCCACCGAAGAA  
TCTTCCGAAGAAAATGTCAACTTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG  
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG  
CGGGGCGGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA  
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC  
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA  
GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC  
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTACCCGAA  
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTG  
CTAGAGCTCTTTAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAAGTTCTAACAGGTTTA  
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC  
CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGAGT  
GAACTTTTCCAAAATTTCTGGAAATGTTAACCTCACCTACAGATGAAGATAATAGAGCAA  
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG  
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74\_17000057519457\_H  
CACAAGAGCCCTTCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT  
AACCACCTACAGGCCGGAAGTGTCCGGGGTGGACGCATTTCGGGTAGCCGAAGAAGTCCCA  
GGATTGCCGAAGAAGTCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTCCTCAG  
AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA  
CGCCGCGGATGGCGAGGAGCCCGCCCGGAGGCTGAGGCTCTGGCCGAGCCCGGGAGC  
GGAGCAGCCGCTTCTTGAGCGGCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGT  
TCCGTGGCCGCTTCCAGGGCCGCGCGGCTGATCAAGCACCGCTTCCCAAGGGCTACC  
GGCACCCGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGCCCGGGCGC  
TCCTCCGCTGTGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTGTGGACTATGCTT  
CCAAGTCTTATATATGAAGAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGT  
CCACTATGGAGACTGAAAAAATCCCCAGGGTCTCTCCAAGTATAGCCAAGACAATTGGGC

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## FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACA  
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT  
TCATTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC  
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCAGCT  
CCTCCAAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA  
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT  
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG  
ATATTTTAAAGTGGTATGTGATCGTGTCTATTATCATCTGCACTTCACTCAAGAGCTTACT  
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT  
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA  
GAACATTATTCTCTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC  
GCTGAGCTTACTGGCCCTCTAACCAGTGTTTTTTTTTTGTTGTTGTTGTGTACATGTTAT  
ATTTATTTTGAACACAGTTTAAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA  
CAGCATGGAAAATATCAGTGTATTGTTTTATGAAACTTTACGTGTATATATAGACCAAG  
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTTTTCAGGGTCATGATCAAAAAATG  
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC  
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA  
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAAACTGAGTTGAT  
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA  
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAAACTGAGTGTGGATGCAAAGTACCAGGA  
GCTAGCTTTTAACTTGCCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG  
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCTTGTAACTCCAATCAACAAACA  
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCCTGTTGGGTATTGGGTACTTGGCACCCCT  
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCCTTTTGTAAAGAT  
ATTTATTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA  
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT  
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCATCACACACTCTC  
AGTTTTGGTATTTTGTGTTTTTGTTTTTATTTCATCTCAAAGTATTTTCTAATTTCCCTTG  
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTTAATTTCCACACATTTGTAA  
TGTTCCAATTTTCTTTTGTATTGCGAGCTTCATTCCATTGTGTTTCAGAGATGATACAG  
TCAGTGCTGTTCTTATGAAGCAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT  
TCATTACCAACAGTCAGCATGCCCCAAGTGCCCGAGCATGGGGCGGATGGCCAGGAATGAG  
TGAAAACCTTCCCTTCTGCGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT  
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTATATTGGATCTAAAATAACTCTTA  
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTGT  
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA  
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA  
TAACATTATTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT  
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGTGTAATAAGGCTAGTA  
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAATCCCTAGT

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CTGGTGCAGCAGGCGCCGAGGCGCGTTCCTGGCCGCTTCCAGGGCCGCGCGGCC  
GTGGTGAAGCACCGCTTCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC  
CGTCGGCGGACGGTGCAGGAGGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT  
GCCCCAGTCGTCTTCTTTGTGGAATATGCGTCTAACTGCTTATATATGGAAGAAATCGAA  
GACTCGGTGACTGTTTCGGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG  
TGCCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC  
CTCATTACGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCTGGCGCAGCTG  
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC



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## FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG  
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG  
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGAGCTGT  
GGTGAAC TGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG  
GGTTGTTAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG  
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCCAGGCTAGCCT  
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGAAGAGGTTATAAGCCACCATACT  
GACTTTGCACTGATTCTGTGAGAAAC

SEQ ID NO: 76\_17000139801197\_H, IRAKM\_H  
ATGGCGGGGAAC TGTGGGGCCGCGCGCTGTGCGGCACACGCTGCTGTTGACCTG  
CCGCCCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC  
TGGCGCGGCTGGCAGAGAGCTTTCAAGCAGCTGGCTGGATGTTTCGT CATATTGAAAAG  
TATGTAGACCAAGGTAAAAGTGAACAAGAGAATTACTTTGGTCTGGGCACAGAAAAAC  
AAGACCATCGGTGACCTTTTACAGGTCTCCAGGAGATGGGACATCGTCGAGCTATTCAT  
TTAATTACAACTATGGAGCAGTGTGAGTCTTCAGAGAAGAGTTATCAGGAAGGTGGA  
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCCT  
GAACATAATGAAAAAGGAGTACTGCTTAAATCTCCATCAGCTTTCAAATATCATAGAA  
GGAAGTAGAAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTGGAGGTATAC  
AGAGTGGAGATTCAAACCTAACATATGCTGTCAAATTATTTAAACAGGAGAAAAAATG  
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTACTACTGTTTCAT  
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT  
TATCCATACATGAGAAATGGAACACTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC  
CCACTCCCTTGGCACATTGCAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC  
CTGCACAACGTTCAACCATGCTCGGT CATCTGTGGCAGTATATCAAGTGCAAAACATCCTT  
TTGGATGATCAGTTTCAACCCAACTAACTGATTTTGCCATGGCACACTTCCGGTCCCAC  
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC  
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT  
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAACAT  
ATCCAGCTGCGGGATCTCCTTAGAGAAATGATGGAGAAGAGAGGCTGGATT CATGTCTC  
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT  
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA  
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGTGCTGAAGATCCTCCCACATCACTA  
AAGTCTTCAGGTGTCCTTCTCCTCTATTCTTGAGAAATGTACCAAGTATTCCAGTGGAA  
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA  
ATGACTCAGAAAACCTCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC  
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCCAGTTCTTCTTGTGAA  
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT  
ATAGATCCTTCTTCAGAAGCTCCAGGGCATTCTTGCAAGGAGCAGGCCAGTGGAGAGCAGC  
TGTTCTCCAAATTTTCTGGGATGAATATGAACAGTACAAAAAAGAATAA

SEQ ID NO: 77\_AA840598\_M IRAKM\_M  
ATGTGGAAGAGATTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA  
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG  
AGCAACGGGACGCTTTTCGACAGATTACAGTGCACAAATGGCACAACCCCGCTTTCCTGG  
CACGTTGCAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAACACT  
CAGCCGTGCGCCGT CATCTGTGGCAACGTTTCCAGTGCAAACATACTCTGGATGACCAG  
CTCCAACCCAACTAACGGATTTTGTGCTGAGCGCACTTCCGACCCAATCTAGAGCAGCAG  
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC  
 ATGGAGGTTCTAACGGGCTGCAAAGTGGTGTCTGGATGACCCGAAACACGTTCTAGCTGCGG  
 GACCTCCTCATGGAAGTATGGAGAAAAGAGGCCTAGACTCCTGCCTGTCCTTCTTAGAC  
 AGGAAGATACCACCCTGTCCTCGGAACCTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG  
 TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG  
 AGCACCAGCCTAGCTTGTATTTTGCAGAAGACCCTCCCACGTCCTTGAAGTCCTTCAGG  
 TGTCTTCTCCACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC  
 CAGAATAACCATTTCAGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGAAGTCTCAGAA  
 ACCCCTTTGAATGCAGCCAGTCTGAGGTCACCTTTCTAGGCTTGGACCGAAACAGAGGG  
 AACAGGGGAAGTGAAGCGGATTGCAACGTGCCCAGTTCTTCTCATGAGGAATGCTGGTCC  
 CCAGAGCTTGTGGCGCCATCCCAGGACTTAAGTCTTACTGTGATCAGTTTGGGCTCGTCT  
 TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG  
 CTCTTTTGCAGTGAGCATGAACAGTCCAAAAGCAGTGAATCCACCAGAAGATCAAGCAA  
 AAAATAAAAGCAAACGTCACTGAAGGCATGAGCAAAATAGCATCCCCGTGAAAAGACACG  
 AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG  
 ATTAGCAGCAAGGAAGTCTATTCCTTCTCCAAACAGAATAATTTCAAGAGATGCTTTAT  
 TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC  
 AAGATTCCGGGTCTTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT  
 AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA  
 CCCACCTTCCAGAACCAGAACCACCTTCTCCCAAGCCAGCAGTCACTCACTCACCATCA  
 GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC  
 CTACGTCCTTTATAAAACCCAGGTCTTCAGGGCCCCACCCCTTTCTTTTCCATCCTTGCT  
 CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA  
 TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTCAGATCATTTGCACAAGAACA  
 AGCGAATACACAACAACAAAGCCCACCATCATTACCACCGGCACTTAATGCTAGTCTTTT  
 TGCTAGGGATACTGACAGTCTATTTGCTTCCCATGGTTCATAGGGAAGTTGCTCAAATGCA  
 AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT  
 TTTTACAGCCAGTTGCTACTCTTGTATATCGCTGGTTAACCAGTCTGTCCGGAAGTGAGC  
 CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCAGTCCAAAGTCTGCT  
 TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAA  
 TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78\_AA088547\_H

ATGGCGAGTGCGGTGAGGGGTCGAGGCCGTGGCCCCGGCTGGGGCTCCAGCTCCAGTTC  
 GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTCTACTCTCAGGCCAGAGAACCTC  
 CTGCTGGTGTCCACCTTGGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG  
 AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC  
 TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA  
 TTAATGAAACTGCCATTACCATCCCTGAGCTGGTTCATGCCTCTCCCTGCCGCAGCTCT  
 GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA  
 GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC  
 CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC  
 ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC  
 CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGTCTG  
 TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG  
 CGCCAGCTGCCGCATCTCACGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG  
 GGCCACATCCGACTGCCTGCCTCAGGCCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG  
 GACACCCAGCTGCTAATGACGCTGTATGTGGGGAAGGATGAACTGGCTTCTATGTCTCT  
 AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA  
 GATGGCCCCACCAAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

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## FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT  
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCACCTG  
GGGAGTGGAACTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG  
GAGCTATTGAGCTTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA  
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT  
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG  
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCCAGTCCCTGCACTCG  
GGGGCCAGCCGGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCCAGCCACTC  
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCCCTTCAATCCCAAGGAC  
GTGCTGGGCCCGGGGCGAGGCGGGACTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA  
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGAAGTTCAACTG  
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCGAGCGGGGACCC  
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCTCCTTGCAGGAGTACGTAGAAAAC  
CCGGACCTGGATCGCGGGGGTCTGGAGCCCGAGGTGCTGCTGCAGCAGCTGATGTCTGGC  
CTGGCCACCTGCACTCTTTACACATAGTGCACCGGGACCTGAAGCCAGGAAATATTCTC  
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCTCAGACTTCGGCCTCTGC  
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA  
GGCTGGATGGCGCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCTTACCAGCGCTGTG  
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT  
GGAGACAGTCTTTATCGCCAGGCAAACTCCTCACAGGGGCTCCCTGTCTGGCTCACCTG  
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTGGAGCCATGTTGAGCCCA  
CTGCCGAGCCACGCCCCCTCTGCCCCCAGGTGCTGGCCACCCCTTCTTTTGGAGCAGA  
GCCAAGCAACTCCAGTTCTTCCAGGACGTGCTGACTGGCTGGAGAAGGAGTCCGAGCAG  
GAGCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC  
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCTTATAAGGGGACA  
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA  
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC  
CGCTTCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC  
CTCTTCCCTGCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA  
GGGAGGTGA

SEQ ID NO: 79\_HGP\_6644466

GGAGGGTTTGAATTGCAACGGCAGCTGCCGGCGTATGTGTTGGTGTCTAGAGGCAGCTGC  
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT  
TTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAA  
GGAAGGGATCAGTAATTTCAAGACACCAAGCAATTATCAGAAAAAAGAAATCTGTATT  
ATGTTCAACTCCAATAATAATATCCCGGCTCTCCGTTTATGCAGAAGCTTGGCTTTGG  
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG  
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG  
ACTAATGGATGAAGCTAAGATTTTGAAGGCTTCATCATCCAAACATTGTTGGTTATCG  
TGCTTTTACTGAAGCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA  
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC  
CATAATTTTAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA  
GAAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAGGCGATTTTGAAC  
AATTAATACTGTGATGTAGGAGTCTCTTACCCTGGATGAAAAATATGACTGTGACTGA  
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCCAAGAGCTGTGGAGGAGAA  
TGGTGTATTACTGACAAGGCAGACATATTTGCCCTTTGGCCTTACTTTGTGGGAAATGAT  
GACTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGAAGATAAACTTT  
TGATGAAAGTGATTTTGATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT  
TAATATGGAAGAACTGGATGAATCATAACGAAAGTAATTGAACTCTTCTGTATGCAC

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## FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA  
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGGCTAAATAACTGTTTATTCCAAAATA  
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG  
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG  
CACTTGGAAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG  
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAAACATTAAAT  
TGAATGACCATTACTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAATGGATCTA  
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC  
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA  
GTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGGATCTCCTC  
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAAATTTA  
TTAATTTGTACCTTAAGCATTTCAGCTGTGTAAAAACAATAAACTCAAATAGGATGA  
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

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ATCTCCAAGAGGGTTGTCTCATTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA  
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAAA  
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT  
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA  
CAAAGACAGTGGAAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC  
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC  
AAATGTTGTAATTAAGGTGATTTTGAACAATTAATCTGTGATGTAGGAGTCTCTCT  
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC  
ATGGAAACCCAAGGAAGCGTTTGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT  
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCATCTTCC  
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA  
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA  
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC  
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA  
TTAACTTGTATGGGAAGTGTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG  
ATTCTAGAAGTAGCTTTAACACTAGTGACCCCTGTCTAAGATGACTTAAGAATCAAGGGA  
CCATTGCTTTGTACAGATCTTTTATGATATTCTTGTCTTCTTAGTGGGTACTAAAAAT  
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTTCAGCTGGC  
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTCATAAACGTAGCTCCTAGGGTGTG  
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT  
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTTAGTACCAGG

SEQ ID NO: 81\_5R57\_10\_2\_M TESK2\_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT  
AGCAGTGGGCCTCAGCTACCTTCACTTCAAAGGCATTTTCCATCGGGACCTCACATCAA  
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82\_AA232253\_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAAATTAAATTTGATGACTTGCAGTTTTTTGAA  
AACTGCGGTGGAGGAAGTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAG  
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCTC  
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATCTTGAACCTCCCAACTATGGCATT  
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG  
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT  
TTACATATGGAGGCTCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTT

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## FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAACCAT  
ACAACACACATGTCCTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT  
CTCCCTGTGTCAGAACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTA  
ACAAGGGAGGTCCCCCTTTAAAGGTTTGGAAAGGATTACAAGTAGCTTGGCTTGTAGTGAA  
AAAAACGAGAGATTAACCATTTCCAAGCAGTTGCCCCAGAAGTTTGTGCTGAACTGTTACAT  
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTCAATCCTG  
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAACCTATTCTACACAACAAG  
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT  
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA  
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCTTTGAGATTGGTGCATGGACG  
GAAGACGATGTGTATTGGTGGGTTCAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG  
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG  
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACTTC  
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAAATTTGTTTCACTTCCCACCACTA  
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAAGTG  
GTTTTTGGTTTTCACTTGAAACCAGGAAGTGGCCACAGGATTGTAAGTGGAAGATGTAT  
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACACT  
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTGTAATGGAGAAGTGG  
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCACGTGTCACATATGAGAGTGATGTT  
AGAAGTCCAAAAAGCACTAAACATGTCCATTGATTGAGTGGAGTAGAACAACCTCAG  
GATGAAGTGAAAGCAGTCCAACCTTGCCATTGAGACATTATTCACCAATTCAGATGGCAAC  
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG  
CAGATTGCATCCAACACTTCTTTACAGCGTTCCCAGAGCAATCCTATTCTGGGGTCAACCG  
TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG  
CCCATTAAAGTATCAACAGATTACACCTGTGAACCAGTCCAGAAGCTCGTCTCCTACTCAG  
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC  
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGATACTCAGACAGAAGCAGGAACAAA  
TATGGACGTGGTAGTATATCACTCAATTCTTCTCCTAGAGGAAGATACAGTGGAAAGAGT  
CAGCATTCCATCCATCAAGAGGAAGATACCCTGGAAGTTCTACAGGGTTTCTCAGTCA  
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC  
AACACCATAACAGGGATGCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC  
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGAATAACCGGAAAAGCCCCACAGGCCA  
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT  
TGA

SEQ ID NO: 83\_AI375137\_H

ATGGGAAATTATAAATCTAGACCAACCCAACTTGTACTGATGAATGGAAGAAAAAGTC  
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAAA  
GAACTGACAGAACTAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA  
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG  
AAATCACATATTGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT  
GGATTTACAGCCTTGCATTTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG  
CTTCACAGTGGAGCTGATATACAGCAGGTGGATACGGTGGCCTCACTGCCCTCCATATT  
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC  
AATATTCAAGATGCAGTTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA  
CAGGTAACCTCGCCTTCTTTTGAATTTGGTGTGCTGATGTAATGTAAGTGGTGAAGTTGGA  
GATAGACCCCTCCACCTAGCATCTGCAAAAGGATTCTTGAATATTGCAAACTCTTGATG  
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCCTCCAT  
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTGGAA  
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAAT

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FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG  
GAAAACATCTTCAGTGAAACAGCTTTTTCATAGTGCTTGTACCTATGGCAAGAGCATTGAC  
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG  
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTCGCCTGGTTCAGTTCTTACTG  
GATAATGGAGCTGATATGAATCTAGTGGCTTGTGATCCCAGCAGGTCTAGTGGTGAAAAA  
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTACACTC  
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA  
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGCGGAAGATTAAAAGCATGACAAAA  
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTCCATCTTCAGCTC  
TCAGAAATTGAGTTCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA  
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG  
TCAGATGTGGATATGTTTGGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC  
GTAATTGAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA  
TACATATCAGGGGGTTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTG  
CAGTCTAAATTAATTATTGAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG  
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG  
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC  
ATGACAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACGCAGTGCCT  
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT  
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC  
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA  
GGGTGGAACGCATGTCTGAAGGAAGACCCGAATTTTCTGAAGTTGTGATGAAGTTAGAA  
GAGTGTCTCTGCAACATTGAGCTGATGTCTCTGCTCATCAAGTAACAGCAGTGGGTCTCTC  
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG  
GCAGCATTAAAGAAGTCGTTTCGAATTGGAATATGCTCTAAATGCAAGGTCCTATGCTGCT  
TTGTCCCAAAGTGCTGGACAATATTCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA  
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG  
CATTTTCAATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

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ATGATTTCTTGCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA  
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCCTGTATTCTTTTTCAAAGTGCC  
GAAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC  
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAACGTGTGGGGC  
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGGAAACAGAGTGAAAAGCTGAGACA  
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT  
GAACCTGGTGCCTGCACTGCCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG  
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAGGAGAATGAGTTGTA  
TGAATCATTGATGAATATTGCCAACCGAAAGCAGGAGGAAATGAAGGATATGATTGTTGA  
GACACTTAATACCATGAAGGAGGAACCTTCTGGATGATGCTACTAACATGGAGTTTAAAGA  
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG  
ACAGATCCAGGAACTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG  
CTCAGTGGATTACCTGAGGGAAAGCTTCGTGCGAACCCCTGGAACGATGTCTGCAGAGCCT  
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACCAGTAATTATCTCAAACAGATCTTAAA  
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCGTGAGTTACAAGGATGCTATG  
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCCACCTGCCATCACTCT  
GGAATGGAAGAGGAAGGTGGCCCAAGGACCATTTGAGAGCCTCAGCGCCTCCAAATTGGC  
TAAGAGCATTTGACAGCAATTCGGGACTCGGCTCAATAGTTCACACGAGGCTTTTGCAGC  
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGCTTAGAGAAAAAGGAAGATCTATG  
GCTGAGGGTTGCGAAAGATCATGCTCCCCGCCTGGCCCCGCTTTCTCTGGAAGCCGTTG

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## FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCCA  
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCTCAAATC  
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG  
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTTCACTATTGACTACAACCTA  
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA  
CACAGGGCTGAAGGCTGGGCTGACCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT  
GGAGGGAATCCGCTTCTGACAGCCAGGCACTTGTCCATCGTGATATCAAACCTGAAAAA  
TGTGCTGCTGGATAAGCAGAACCGTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA  
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCTGAACTTTTCAC  
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGAAATTCCTTTCTGGTATATCTG  
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG  
GAACAATGTGCGGAGGGGGGCTCGCCCAAGACGCTTCTCTGTGTTTGATGAGGAGTGCTG  
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTTGGGCATTGT  
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA  
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT  
TCCTTCCCCCTCACCATTGCGCCATGGGGAGAAATTTGACATTTATTCACTATAGGACACA  
CTCCCAAGGGAACCTGGTGCTTGTGCTGGGAAACTTGAACCTTCCAGGCAGGGATGACTCC  
TGGACAGTGAAGAGTTGAATGACTGAGCATATTGAGCAGCTCACTGAAGCGCCAAGCTAT  
CCCTTTAGCAAAAAGTGTCTCAGATGTGTAAAAGCTGAGGAATGTGGTGTCTTGGCTTC  
ACAAATGAAAAGGAGGCAGATGTT

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TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT  
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA  
CAGTGTGTGACAGGCAGAGTCGTCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA  
CTCCCGGCTTGGA AAAA ACTGAAGGAGTTAATGATTATTGCTGGGGTTCCAGTCCGAAA  
ACAGGCCATCCTTCCAGGACTGCGAACC AAAA ACCAATGAAGTTTACAATCTGGTAAAGG  
ACAAGGTAGATGCTGTCTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG  
GCAGAACTTGTCTGCCAGAGAGCCAAGCCAAAGAGGCACAGAAATGGATTGCCCGAGGG  
AAACCATGGTTTCTAAAATGCTGGACCGCCTGCATTGAGGAAACCTCCGGACCAAGTTC  
CTGGA AAATGTCCTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA  
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCTTCAGAG  
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACCCCAAAGGAATCAGG  
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCCAACGAATCCAATGACAGGGC  
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCTTGG  
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTTCGGCA  
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA  
AGTGTGCCATTGAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC  
AGTCCTTGCCACTTCCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAA  
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTAACTGTG

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ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACTGAGAGAACCACCATTTACCTTA  
CCCTCTGGACTTGCTGTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT  
GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTGGAAGCACTT  
CGTCACCTTGCTTGCTAAGATTTTTATCTTGTAAGTGTGGAAGCGGATGGCATTCTCTT  
GTCACTGAGCGAGTACAGCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC  
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCCCTTCATGACAGAGGACACCTA  
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGCACTGGAAGCTA  
GGAGGAATGGAACCTGTTTGTAAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

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## FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAACT  
CTCCCAGAGTGTCTATGGACATGCCCGGGATGCCTTTTTCATTTGGAACATTGGTGGAAAGT  
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC  
TTGCACTCAACTTTGCTGAATCCCATTCCAAAATGTCTGGCCAGCGCTCTGCACCTTACTA  
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAACA  
TTGAAGAGTGAAGAGGAGAAAACGGAATTCTTTAAATTTCTGCTGGACAGAGTCAAGTGC  
TTGTCAGAGGAATTGATAGCTTCAAGGTTGGTGCCTCTTCTGCTTAATCAGTTGGTGTTT  
GCAGAGCCAGTGGCTGTTAAGAGTTTCTTCCCTTATCTGCTTGGCCCCAAAAAAGATCAT  
GCGCAGGGAGAACTCCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC  
GTGCTTCTCCAGTTGTTTGAAGTTTCATGAAGAGCATGTGCGGATGGTGTCTGTCTCAC  
ATCGAGGCCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG  
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA  
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAAACGAACCAAGATC  
TTCAAACGCACTGCCCCAAGTTTTACTAAAAATACTGACCTTTCTCTAGAAGGCGATCCA  
TTTTCTCAGCCTATTAAATTTCCCATAAATGGACTCTCAGATGTAAAAATACTTCGGAG  
GACAGTGAAAACCTCCCATCAAGTTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA  
CCTGAGGAGCCTGAAAATCAAACCTGTCAACATACAGATTTGGCCTAGAGAACCTTGAT  
GATGTCAAGTCCAGTGCCTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG  
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT  
ACCTCAGGGGAGCAGAAGCCTATTCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT  
TGGAATCAAGCTTACCCCCAAAAGATTAGCCTTGTACAAAGGGGGGATGACGCAGACCAA  
ATCGAGCCGCCAAAAGTGTCTACAAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT  
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAGATCCTGAGATGGAT  
TGGTTTGCTGATATGATCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA  
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCCAGTGATGCAGTTTCTCTCA  
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG  
CTGAACCTGGGAAGATAATAACTGGTGA

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AGCGGCCGCGGGGGCGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA  
GGCAGAGCAGGAACAGCCAGGAGGCGTTTATTAGGGGGGCGGGGGGAAAGAGCCCCAGCA  
CCGCCCCCTCTGGAAGAAGGAAGAGGTAACTATACTACCCAATATTGCAGCCATGGAGT  
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCGG  
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTTCGACACATTGCCAGTGGTTGCA  
ATGGGCTAGCTTGGAAAGATTTTAAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG  
TTTTTGCTCTTTGATAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA  
TTGATTCTCTAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA  
CTGTCCAGCATCCTTTAGAAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAGTTT  
TTGCCAGTTTAGCCAATGTTCTTGGTAACTGGGAAAATCTACCTTCCCCTATATCTCCAG  
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGCTTCAGGTTTCTG  
AAGGATTGTCAATTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA  
ATATAATTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT  
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCAAATTTAC  
CTTCATTGTGTCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT  
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG  
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG  
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTTCGTGAAC  
AGATTCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC  
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAC

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## FIGURE 2RRR

TGCCCAAGCGTGTTCATTGTGCAGAGAATTTTGCCCTTGTTGACTTCAGAATTTGTAAACC  
CTGACATGGTACCTTTTGTGTTTGCCTAATGTTCTACTTATTGCTGAGGAATGCACCAAAG  
AAGAATATGTCAAATTAATTCTTCTGAACTTGCCCTGTGTTTAAGCAGCAGGAGCCAA  
TCCAGATTTTGTTAATTTTCTACAAAAAATGGATTGCTACTAACCAAAACCCCTCCTG  
ATGAGATAAAGAACAGTGTCTACCCATGGTTTACAGAGCACTAGAAGCTCCTTCCATTC  
AGATCCAGGAGCTCTGTCTAAACATCATTTCCAACCTTTGCAAATCTTATAGACTACCCAT  
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC  
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

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GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG  
GACCCGGAGCTAAGGCGCCCCGAACCCGCGGCGGCGGTGGGGACGATGTGGTTCTTTGCCC  
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGGAGCCCCCAGAGGGCGGCCTGC  
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT  
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA  
AGCGCTTCAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG  
AAAAATGCCTCCACGTCTGTGACAGAGGCTGTGACCCCGTTGGGAATATACCTCAAGGCGA  
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGGCTACACCAGATCGTGA  
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG  
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCCG  
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC  
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT  
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGCCCCTACCTCGGGCAGCAGCCC  
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCCATTACTGTGAGCTGGTGGGAG  
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTGTCAGAACTGCCGGGCACCTGGTG  
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATTAGATCAAAG  
AGCCAGCCGAGAAGCAAAAATCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG  
AGGATTTCTGTGCGGCACAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG  
CTGGGGCCGTTGTCTCACGCCCCCTCTTCAAGGTGGGCAAGTTCTGAGCGCTGAGGAGT  
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC  
GCATCCGCCTCCTGCAGCAGATGGAGCAGTTTCATCCAGTACCTTGACGAGCCAACAGTCA  
ACACCCAGATCTTCCCCCACGTGCTACATGGCTTCTTGACACCAACCCTGCCATCCGGG  
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG  
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT  
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA  
GGGTCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGACCCGTCCCGGGTTG  
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCAGA  
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG  
CCTTCAAGGCCATTTCGGAGCTTCTGTCCAAATTTGGAGTCTGTGTGCGAGGACCCGACCC  
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG  
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC  
GTTTCGCACCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG  
GAGTTCCTGCCCCAGCCCCCACCCTGTTCTTGCCACCCCTACAACCTCAGGCCACTGGG  
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG  
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCAGCAGGACGACT  
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGTGAGCAACTCCGACCACAAATCCT  
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT  
GGCAGGAGCCAAGCTCCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA  
ACTGGGGTGGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC  
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

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## FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCGGAAGAAGCGCGAGGAGCGGCGGGGAGA  
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA  
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGCTGCGGAGAGCCCGCCCCACAGATGT  
ATTTATTGTACAAACCATGTEAGCCCTGGCCGGCCAGCCAGGCCATCTCACGTGTACATA  
ATCAGAGCCACAATAAATTCTATTTTAC

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ATGGCCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG  
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG  
CAAGGAGGAATTTCTGTGAAAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT  
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCCTCCCCAAAAAATTG  
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC  
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT  
CCAAACAACCTATTCCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTTCCATGTTCTTC  
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACCTTTGAAAGACATAGGTTGGAGAATAAGG  
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTTAAGCTGG  
GCTGACCTTGCGCCAGACAAGTATTTGTGAGATAAAGATTTTCAGTGTCTAATCAAACCTT  
CTGCCTTCTTGTGTTGACCCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC  
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG  
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTGAGGCGCTG  
GAACTCCAGCAAATAAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT  
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT  
TGCCCGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCTTCTACCGATCTTAT  
TTTTTACAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTTGCCAC  
TTACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCCT  
CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT  
AAAAATGGCATGCCTACCATCTCCCGCTCTTACAGATGCCATTATTGAGCGATGTTTTA  
CTAACCCTTCTGAAAAACACAGTTTAAAGATCCCTACAAAGTTAAAAGAGGCATTGAGA  
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTACCCAGCAT  
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG  
ATTTTAGCTCGAAAGAAGTCAAAACGATCTGCTCTTGAATAAGTGAAGAGCATTGAGCG  
AAGTACAGCAACTCCAATAATTGAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG  
TCATCGCCAACCTCACCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT  
CCACCACCACCAGCAGCTCCCTTGCTCCTGCGAGCACCGAGGCACCTGCCCAGCTCTCG  
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCTTGCTCAGCTCCATCCAGAATTTCCAA  
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT  
TCCTGTTTACACTTGAGGGGAAAAGTTCTTTTTTATTCTACTCACCCCTACCCCCAAC  
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC  
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC  
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

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ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC  
TCACAGGCCCTCTGCGGGCCCGAGTCTTGGGCTCCGAACTAGCCCTGGCCACACCGGTG  
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC  
TACTGCAAGGGCGGCTACCAACCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC  
GTGGTGCACAACTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG  
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGGGGGCATTACACGGAGACAGCT  
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCCAAGTACCCCAAAAGA  
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

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## FIGURE 2TTT

TGCATGGTGTCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC  
CAGGGCCTGCCCCGTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC  
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCCGAGAACATCTTGCTG  
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA  
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT  
AAGCTGTCCAAAACAAGAGGAAGAAGATGAGGCGCAAACGGAAAACAGCAGAAGCGGCTG  
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT  
GAGGACTCTGGCTTGAGACTAGACGGGGGACGCGGCTCCACATCCTCTTCAGGCTTCTCC  
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG  
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCGGTGCCTCGAACCTCCTGGTGAACCCC  
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC  
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG  
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC  
GAGCTGGCCACTGGTGA CTACCTGTTTCGAGCCGCATTCTGGAGAAGACTACAGTCGTGAT  
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC  
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT  
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG  
GCCACACAGTTACGCGCCTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC  
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

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TCTGGCCCTGTCCCTCCCCACCACCCGCGCTGTGTCCAGACAGAGAATGTTCTAACGCT  
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGGA  
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC  
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG  
ACCTACTCAAAGTCAAAGAAGCATTTTCCAAAAAACACCAAAGAAAAGTGGCAATTAAA  
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTCCCTCGGGAGCTC  
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT  
GCCGACGGGAAAACTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC  
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGGCCAAGGCCCTCTTCCGTGAGATGGTT  
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC  
GCCTTGTGTCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCC  
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCGAG  
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATCCCCAAGATGCTG  
CTGTATGTATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG  
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG  
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT  
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA  
GTAGGGGGAGAAAGCAA

SEQ ID NO: 92\_AA060026\_M SGK022\_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGCGGGGAAAAGA  
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG  
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC  
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC  
ATCAAAGAAAAGTGGCAATTAAATATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC  
AGAGATTCTGCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAACATCATCC  
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGTATGGAAGTGGCTG  
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA  
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCCC

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## FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTCAGGGCTTCAACCTGAAGCTGACCGACT  
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA  
GCACAGCCTATGCCGCCCCCTGAGGTGCTACAGGGCATAACCCATGATAGCAAGAAAGGTG  
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGT~~T~~ACCTTTTGTATG  
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT  
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC  
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC  
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAACCTG

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CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCGCACTTCATTCTCAA  
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTTCGGAACATGGGACCTTG  
AGGAGTTCCGTAACCAAAAGGAGAAAGTAACAACAGCCAGTGAGACAAAAAGAACTGCT  
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGAGGGCTGAGTCCAGCATCCCAGACTCGT  
GTGACTATATAGGCAAGCATTGGGGACCTACTTCACTTTGATACCCTAGCCTTCAGCAG  
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA  
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACCACAGCCTACC  
ATTCCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG  
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT  
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA  
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC  
GAGTATACATCATTCTGGAAGTGGCTCAGGGTGGTGTATGTCTTGAATGGATCCAGCGCT  
ACGGGGCCTGCTCTGAGCCCCCTTGCTGGCAAGTGGTTCTCCCAGCTGACCCTGGGCATTG  
CCTACCTGCACAGCAAGAGCATCGTGACCCGGGACTTAAAGTTGGAGAACCTGTTGCTGG  
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC  
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTGGCTTTTCCCACCTCAGCCAGA  
CTTACTGTGGCAGCTTTGCTTACGCTTGCCCAGAGATCTTACGAGGCTTGCCCTACAACC  
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTTACACTCTAGTGGTCGCCCATC  
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT  
TCCCAGCTAACCATACCATCTCCCAGGAGTGCAAGGTCCAAGTCTGCTCATTGCCTGTGTGG  
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCCTGCTCTAGAACCTGATCCTCC  
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCTCTGGG  
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC  
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA  
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA  
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94\_AA758539\_H

GACCATTGACAGCGCTCCGGTAGTGTAATGAGGACAAATGCCTGCTGGCCACATGACGG  
GGGGATGTAGACGGCAGCGGCCAGTCTGCTCCTGGCACCATTGGACGATGCCACAGTCCT  
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGCAAGGGTTCCTACGCAAAAGTCAA  
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA  
AACACCTACTGACTTTGTGGAGAGATTCTTCTCGGGAGATGGACATCTGGCAACTGT  
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA  
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC  
CCTGCATGAGGACGTGGCAGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG  
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA  
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG  
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTCCGCAGCATATGCAGCCCCCGAGGTGCT  
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

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## FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT  
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA  
CCTCATCTACCGCATGCTGCAGCCCCGACGTGAGCCAGCGGCTCCACATCGATGAGATCCT  
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCAAGCCACGTCTTCTGCCTCCTTCAAGAG  
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGGC  
CGACCACCGGCCCCGACCACAAGCTTGGAGCCAAACCCAGCACCGGCTGCTGGTGGTGCC  
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA  
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG  
TGGTGGGGGTCGGGGTTGGGGGGCATGGTGCAGTCGGCCTTACGTAAACTAAGTAGGCA  
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAACCACTATTTTGA  
TT

SEQ ID NO: 95\_AA883975\_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCGCACAAATTGGAGAG  
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC  
AAGGTGGTGGACCGGCGGCGAGCGCCCCGGACTTCGTCAACAAGTTCCTGCCGCGAGAG  
CTGTCCATCCTGCGGGGCGTGCGACACCCGCACATCGTGCACGTCTTCGAGTTCATCGAG  
GTGTGCAACGGGAAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC  
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGCGACCTCTTTGCGCAGATCGCC  
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC  
GTGCTGCTGAGCCCCGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG  
GCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCACCC  
GAGGTGCTCCTGGGCATCCCCACGACCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC  
GTGCTCTACGTGATGGTCAACGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG  
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC  
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCCGTCCGCCAGGCCCTCCGCGGGCCAG  
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGGACTCCGGCTAG

SEQ ID NO: 96\_AA905446\_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA  
TCATGGAAAGAAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT  
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC  
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC  
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG  
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC  
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCTTTCTGATCTGCCAGCCCAT  
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCGGGAGCTCCAAAT  
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA  
CGGGAATAATCTGCCTGGTGATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT  
GAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGTGGTTGAGGC  
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT  
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC  
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT  
GCAGGGCATTTCCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGTGTCTTCCCCACTCA  
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT  
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA  
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

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## FIGURE 2WWW

SEQ ID NO: 97\_H29974\_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC  
CGGGCGCAGCGGGGCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT  
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT  
CGTGCAGTTTGAGGAGTGCCTGTCAGCGCAATGGGTTAGCCAGCGCATGAGTCACGG  
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT  
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTCTATGGAGTTCTGTGAAGGTGG  
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT  
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT  
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA  
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGA  
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTCTGGACTTCTA  
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG  
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA  
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT  
AGAAAACCCAAAGATGGAGTTGCACATCCCCCAAAAACGCAGGACTTCCATGTCTGAGGG  
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT  
TGAAGTTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAATTCAGGGCTAAGCAT  
TTTGGGTGATTTTAAACTAGGTGATTCCTCGGGACCCACAGTCTCACCACGTCTCCTCC  
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGCTTGGCGATCTCCCGACAGCTGGA  
TCCGGCAATGTGAAGCTTTTGTGGGTTTCCCCGCTTCTTTTTTAGTTTTGCTTTATTN  
TNCCCTTTTCTTTTCTTTTTTNTTNNCCACNTNCCTTTTTTTAAATTTAAACCATTGAG  
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA  
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT  
TTTTGGTTTTGTCTTCACTTTCCCTCTGTCTTCTTTATACTTTTCTCAGTTCTAC  
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT  
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG  
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA  
GAGGTGAAGAACCGCC

SEQ ID NO: 98\_AA498104\_M H29974\_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCGC  
AGAGGGACAAAAAGCCCCGAGCGGAAAAGGCGAAGCCAGTCCAGCGGGTACTGTGCGAG  
AAGCTGAGGCGCGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC  
TTCTTGGCCCCGCGCGGCCGATGGCGGCGGCGGGGATGTTCTGTCACGGCCGCGCTAC  
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG  
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG  
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG  
CAGTTTGAGGAGTGCCTCTACAGCGCAACGGGTAGCCCAGCGCATGAGTCACGGCAAC  
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG  
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTCTATGGAGTACTGTGAAGGTGGAGAC  
CTCAATCAGTATGTCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTCATGCTA  
CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAAACCACATCGTGCACAGGGACCTAAAG  
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT  
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCGAGGCAAAGAGGGCAATCAAGATAAC  
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG  
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT  
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC  
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCTAGAA  
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTCT

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## FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA  
CTTGAAACCCGAATGGACCAGGTACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG  
GGTGTTTTAAACTAGGTGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA  
TGGCAGAGGGTACAGGTGGTGGTGTATCTCTGACAGCTGGACCTCCCAACAATGTGAAGCT  
CACGCTTGGGCTGCCCCTCTACCTTCTCTTCTCCTTCAGTAGAATAATAATTGTTTT  
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99\_AA215311\_H

CGRCCGCGCTACGGAAAGCCGGAGGGGGCGGGGCCGTGCGCGTAAGGGGGTGTGTCCGC  
GCGCACCACGGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGAGCGGAGGCGCGAGC  
TGCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA  
GAAACCTCGACCTTGAAGATGGTGTAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA  
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG  
GCAGTGAAGAAAATTCGATGTCACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC  
TGGGCACTAAGCAGTATCAAGAGCCAACATCCAAATGTGATTCACTTGGAGGAATGCATC  
CTACAAAAGGATGGGATGGTGCAAAGATGTCCCACGGCTCTAATTCTTCCCTTTATTTA  
CAGCTTGTAGAACTTCATTAAAAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT  
TTGTGGTTTGTGATGGATTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG  
AAGCCCAATCGTAAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC  
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA  
ACCAGGTGGGATACCAGTGACTTGAACCTACCCTCAAAGTGGCTGATTTTGGTCTAAGT  
AAAGTTTGTTCAGCCTCTGGGCAGAACCCAGAAGAACCTGTGAGTGTAACAAGTGTTC  
CTTTCCACAGCATGTGGAACAGATTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC  
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAGGATC  
ACATTATAGACACAGAGACAAAGAAGGAACCTTGGGGAGTTATGTAAAACAAGGAAC  
GAGATTGTGCCTGTTGGGAGGCACTTCTGGAATAATCCCAAAATGGAACCTTCTCATTCC  
GTGAAGAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA  
AACCTCAGGATCGTCCAGATGCTTTTGAACCTAGAACTCAGATTAGTACAAATTGCATTT  
AAAGATAGCAGCTGGGAAACGTGACACATATTATTGCAAATACCATGGATGATATGCTG  
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAATATAAAAAGCTAGACTC  
TACCCTCTAAGGGTTTAGATTTTTTGTGGGATTTTTTTTTTCTCATTCTTAAATCC  
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT  
AAAAAATGATTATTGATAGAAGTTTGGCAGGAAAAATCTTTAAGAGCTAACAGAGAAGA  
GAGTCCAGTTTTCTGGAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG  
AATTTCCATGGGAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAACTTTGTAAAGG  
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC  
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGTAGATT  
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCCTACTCTGCCCTCCC  
CCTAATGAAATCATATTAAGTNGTTTTTCCCTNNTTTTTTTTGTAATATACAGCTTTTTTTT  
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAACAAATGAAATTAAGTGATCC  
AAAGCTGCTGAAGTATGTTTGAACCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT  
CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100\_AA018361\_H

GCGGGGCGCTCCGTATCCCCACGTGGGCCCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG  
AGGCCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC  
TGCAATTTCCGGCGGGCGGCGCTGGGGGCGAGCTGGAGCCACCCAGTGCTCGGCCCGCCCC  
GCAACCCGCGGGAACCGCCGCCCGCAGCGAGGAAGCGCCCGCGGGGCGCAGGCGGCCGG  
AATGGCGGGGCGCGGCTGGGGTCCCCCGCGCCTGGACGGCTTCATCCTCACCAGCGCCT  
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

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## FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT  
CACGGAGATTGAGATCCTCAAGGGCATTTCGACATCCCCACATTGTGCAGCTGAAAGACTT  
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTGCGCAGGGGGCGACCTGTC  
TCGCTTCATCCATAACCGCAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA  
ATTAGCTAGCGCCCTGCAATTCCTGCATGAACGGAATATCTCTCACCTGGATCTGAAGCC  
ACAGAACATTCTACTGAGCTCCTTGAGAAGCCCCACCTAAAAGTGGCAGACTTTGGTTT  
CGCACAACACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT  
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCGCGGTGGACCTCTGGTCCATGGG  
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTGCTTCTCGGA  
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCTGCTCTC  
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC  
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG  
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATTCT  
AGCAGCCGCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGCACTA  
TGAAGTGGATGCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG  
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC  
CTCTGCCCGAGACCTGCTCAGAGAGATGGCCCGGGACAAGCCACGCCTCCTAGCTGCCCT  
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCGCCGGCGGGGAGCAGGATGCCCT  
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG  
AGGCGGGAGCTGCTTCACACTGAGGTTTCAAGACCTCATGGCCCGAGCTGAATACTTGAAG  
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGGAA  
TCTGTTTCGTAGCTCTTGCAACCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC  
CATCTGGAGCAGAGGGGCACTAACCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG  
CCCTGGCGAGCAGGCTTCTTGATGGACAGTGTGAGACCCCATATCCCAGAGTCCCCA  
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGATGGCTGTGCTGTATACTGGAG  
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGT  
TACTGGGTCTGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTTGGCTCCGA  
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC  
AGCTGTGCCCTGGCCTGCCCTTCCCGGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA  
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACCCTCCCCACAGTATGCACTCAGCC  
CCACAGAACCACAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG  
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC  
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCTTGGTCTCATCTCTCCACCTCCGTT  
CCCTCTGGGCCCCACACTAGCCACAGCGCGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA  
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC  
CTGCCCTGCCCGCGTGGAGCCCTGGGCAAGCTCTTTCCCTTTCTGGGCCTGGGTCTCCC  
CATCTCTTCAATGGGGCTGATACCTTCACAGCCACAGCATGGGCACCTTATGAGGACAAA  
GTGAATTTAACCTGGAAAAGAATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT  
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCCTTGGGCAAGAGCTGTCTGTCTCTCC  
TGCAGGAGGCTGAGTGTGAAGAGTATCATTATTGTTTCTCTATTAAATTATTTTCTCT

SEQ ID NO: 101\_AA311714\_H

TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT  
GGACTCTTTTCTTGACTTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA  
GAAGTCGGCCAGAGATGGAAAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG  
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTGTAGCCATTCTTTGTACT  
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCTGAAATAAAACAC  
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT  
GAAAACCTCCAGAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGATTACAT  
CATCTTCATAAACTTGGCATTCTCTTTTGTGACATTTCTCCTAGGAAGATACTCTTGAA



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## FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTGTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG  
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC  
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT  
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT  
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTTCAGAAATTAAGTAAAAG  
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCTAAAGCTTCT  
TCAGATTTTATTAATTTGCTTGATGGGTTACTTCAAAGAGATCCTCAGAAAAGATTGACT  
TGGACAAGGCTACTGCAGCATTCTTTTGGGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA  
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTCTGGGCCACAAGAT  
TCCAAGGAGCTTTTGAGAACTCTCAGAGTAGACAAGCAAAGGGCACAAGAGTGGTCAA  
CCACTAGGTCACCTTTTTCAGACTAGAAAATCCAAGTGAAGTTTCGGCCTAAGAGTACTCTT  
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTTCTCGTCTACTCCAGAACTAGC  
ACTGCAGTGGAAAGTAAGTCTGGTGAGGATATGACTCACTGTTCAACAGAAAGACTTCT  
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCAGATGAGA  
GAGCTTATCTACACGGACTCAGATCTTGTGTGACCCCCATTATCGACAATCCAAAGATA  
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCACTG  
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGTGCTCG  
CAGATCGACTCCACTGAGAAGAGCATGGGGGGCCTCCCGAGCCAAGCTGAATCTCCTTTGC  
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG  
TTCCAATTGCTAATCCAGCATTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTT  
GCTCACGTGATTGGTTTACTGGCTTCGCACACAAGTGAAGTCCAGGAAAATACACCTGTT  
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCAACTCCACT  
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA  
AAACTGTATCAGCATT

SEQ ID NO: 102\_SGK384\_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC  
CTGCGGGGCCTGGTCAGCGGCCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103\_AA210451\_M SGK384\_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTTCGGCTGTAGA  
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA  
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA  
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA  
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG  
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTCATCTCCCTGGACGAT  
CCACCGCGGACTCTAGGCGCTGTCCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT  
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG  
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT  
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT  
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATTC  
TCACCGAATATCACCCCTTAGGTTCTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA  
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA  
TCATTAATCTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC  
TGCCCCAAAACATTGTCCAGTACCTGCTAACAAGTAACTTCAGCATTGTGGCAAACGACC  
TGGACGCTCTGCCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG  
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT  
TCCAAGACGATCTCATGCCTTCCTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG  
TCTCCAGTTTCTCTTGGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTTG  
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

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## FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGCAGACGAAAG  
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG  
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTACGCC  
ACGTAGGCCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTCTGCTCTCCTGGCAGCCCCG  
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG  
ATTCTGGATCTGCATAGTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC  
TGCTTTGGTAACTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC  
AACCCACTAGTTCCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG  
GATGTTTTAACTCCGTGGCAGGGCACTTGCTAGTTGTGTGCAAAGCCTTGGATCTGACC  
CATGGCATGTGCACACACAAATGCTCAAAGAAAATCCAGACGCCAGAAAGTGTGCCCC  
TTTCTTGTCAATAAGGTCATTGTTCAGTACCGGAGATGATTTTTTTTATGAAGCGTTTATG  
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTCTTCTTT  
CTTTCTACCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGAGAGAGA  
AAGGAAAGTGGGCACGTGTTATATTGTTGGACGACTTCTTGCTGATTAAGGGGTGTGAGT  
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTTCTTCTTGTCTTCTTCTCGCC  
CACGACCACTTCACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG  
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATTCCAATCATCACACACTCAGAG  
AAACTGTCTGCTGCTGGCAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG  
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAAAAACAAAAACATT  
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG  
AGATTGTGGCTGTCTAGAGATTTTTTGAACAGCAAGTTGAAGGAACCTTTCTTACCTGCCT  
TGAATGGTGTCTTTGAACTTCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT  
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGCATGCCTGAACACTTTAA  
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCAGCACCTGGGAGACAGGAG  
GAACAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC  
CAATAAAAAAACAAAAAGGTC

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GAGGTGGTGGCTGTGCAGATGATGGTGGAAATGCATGGATGACCATTACGCCAGTCAGGCC  
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCACATCTCTGTGTACCAGGAG  
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGTGAGTTT  
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC  
TCTGAGTGGATGCAGAATGTGCTGGGGCAGGTGCTGGACGCGCTGGAATACCTGCACCAT  
TTGGACATCATCCACAGGAATCTCAAACCCCTCCAACATCATCTCATCAGCAGTGACCAC  
TGCAAACTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT  
CGTGCGGAGGAAGACCCCTTTCGTAAGTCTTGATGGCCCTGAAGCCCTCAACTTCTCC  
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC  
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCAGGC  
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC  
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC  
GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCTGTCGTCTCTCTGACCCCTG  
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC  
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC  
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTTATTATTTATGCCCCCTGGCCTTGCTCCAC  
ATGCACGACCAAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC  
TCCCTGGGGAACTAGGGAAGCTGTTGGGCCCCATCCCAAAGGTCTGCCGTGGCCCCCG  
GAGCTGGTGGAGGTGGTGGTACGACCATGGAGCTACATGACAGGGTCCCTCGATGTCCAG  
CTGTGTGCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCAACCCGAA  
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCCCTGCTGAGTGCTCTTCAGAGCCAC  
CCCGAGGAGGAGCCACTTCTTGTGATGGTCTACAGCCTGCTAGCCATCACCACAACCCAG

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## FIGURE 2BBBB

GAGTCAGAGTCACTGTGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG  
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG  
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA  
AACCACGGAAGCCCGGGAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC  
AAGGCCCCCTTGGAGAAGGTCCCGGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG  
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC  
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC  
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG  
TCAGAGCTGGCGGCCTTCAAGGTGGTGGTGACAGGAGGGCGGCAGTGGCCTCAGCCTC  
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG  
CTGCTGGTCCACCTGGCTTCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG  
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTCACCTCCAGCCTGGTGAAGTACAGCAGC  
GCCTTCAGCAAACAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT  
GGGGGACTGGAATAG

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CAGAAGAAGACCCCTGCCAGAAGTCCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT  
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT  
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC  
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT  
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA  
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC  
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAACATCT  
TAGGCAGCTGGCTGTGTGCTTCTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG  
GCTCGCAGAGACTTGGGTTTGATTTTTCAGTCAGTCTCTTGGACAGAGCACCCCTCTGAAAG  
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT  
TGACAAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCACAGAGCTGCTGGAAGAGGTGA  
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC  
TGCTGCGTGTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA  
GTTTGATCATCTCCTTCTGATGGATACCTTGCGGAGCCATCCTAACTCTGAAAGGCTTG  
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC  
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCAAGAGAACCCTGGAGCACTTCCAAGAGGACA  
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG  
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACTGGGTGCTGGCTACTCATC  
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTG  
GCTGCATAAAGGAGAGTCAGTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC  
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA  
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC  
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCTGAGGTGGTGGAGAACCTCT  
GCATGCTGTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG  
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT  
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG  
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCTCTTCAGGC  
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA  
TTTCGTACCCCATGGTGAATAATAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106\_018653.9\_H  
GGCCGGGGTTCGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGCGCAGA  
GCGGAGCCGCCTCGGAGCCTGAGCCGCCCGGGGCGGGGCGGGGAGCCGCGCGGGGCGG  
GCCGCGCGGGGGAGGGGAGCGATGCGGCGCGGGCGGGCGGCAGTGGCCGCGGGTTTCTG

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## FIGURE 2CCCC

CGCCTCCTTCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTCCGAGCCTCCG  
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC  
GGGGAGCTGGCCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG  
GGCCCCGGGCCCCGGGGCGGGCCGGCCGGAGCGGCGGGCGEETGATGGACCTGGCTCCGGGC  
GGGCCCCGGCCTGCCGCGCCCCCGGCCCTTGGGCCCCGGCCCCGTGTCCGACGGCGCCCCA  
GGCTGGCCCCCGGCTCCCGGCCAGGCTCCCCCGGCCCGGGCCGCGCCTGGGCTGCGCC  
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC  
CGGGTCCGCTGCCCGCGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC  
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGCTGCTATCGGCTGGCGGCC  
CACAAGCTGCTTAAGGAGATGGTGCTGCTGGAGCGGCTGCGGCACCCCCAACGTGCTGCAG  
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCACG  
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCCTGGGAGGATCGATT  
CGAATCTGCCTGAGCCTGGGCGCCCTCCTCCACCACCTGGCCCCACTCCCCACTGGGCTCC  
GTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG  
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA  
CTCGAGTTTCCGGCCAGGAACCTTACCCTGCCCTGCTCAGCCCAGGGCTGGTGCGAGGGC  
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT  
CACAGTGCCCCGCCTTCACTGCGTCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG  
CTCGCCTGGGGGGTGGACGAGACCCTGGCCCAGCTGGAGAAGGTGCTGCACCTGTACCGG  
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACAGTGTATCCCA  
GACAGCACCATCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC  
CTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGT  
CGGGCCTTTGTGGTACCAACCAGACCACCTGGACAGGTCCGCAGCTGGTCTTTTTCAAG  
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC  
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCCTGTG  
GAGGGAGTGA CTTGCACTGGCAGCACTGCATGTACCTGGGAACCCCTGCAGACAAAGCT  
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAT  
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT  
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC  
TGTGCCCTCCTTGGGACGGTTCGGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGA  
ATGTAGCTAAAGCCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGTGCG  
TGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG  
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG  
GGGACACTCCAGGCCAGCCAGGGGTGAGGGGCAGAGGTGCACACCTCAGCATGAGCCA  
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAAGCAGGACCTGGGGCGGGGTGGGGCCGG  
GGCCTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC  
CCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTGGTTAAATTGTTTAT  
TTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC  
T

SEQ ID NO: 107\_AA396601\_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG  
GCTACACTAAGGCTGTGTACCGGGTCCGCCTGCCCGGCGGCGCCGCGGTGGCGCTTAAAG  
CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG  
GCTGCTATCGCCTGGCGGCCCAAGCTGCTCAAAGAGATGGTGCTGCTGGAGCGGCTGC  
GGACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG  
ACACGCTGACCACCATCACAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA  
CTTCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCCTCCTCCACCACCTGG  
CCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG  
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCGCGTGGAAGAGACACCGTGCA

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## FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACTTCAGCCTGCCCTGCTCGG  
CCCAGGGCTGGTGCGAGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT  
TCTTACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA  
TCGTCAATGCCACGGGAGAGCTCGEETGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA  
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG  
AGTACCAGCGCATCCCGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT  
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG  
AGAGCCATGCTCAGTGTCGTCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTTCGGA  
AGCTGGTCTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT  
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCCTGCTG  
CAGGCGTGACTTGTCATCCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA  
CTGATGTGACCAGGACAAAACGTGCAATATGAAAAATGTTAAATGTGAGTTTGCCAGC  
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG  
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG  
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC  
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG  
GAGATGTGAGTGAAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC  
CTAGGCCAGCCCCGAGGCCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG  
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTCGGGGCCTCTCTG  
CCTCATTTGCTTTTCAGTGAAAGCCAGGGAGCAGCCGAGCCAGGCTCCTCCACTCCTGG  
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTTCGCTACC  
CAGAAGCTTTTATACCTTCTCGTTCATTAAATTGTTTATTTTGTAAAAAAAATTAAT  
CAATTAATAAAAATGATGTTTTGTGAC

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ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC  
TACTGTGGAAATTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA  
CATGTGTCATCCTTCCAAGGCTCAAAGAGAGGGGCTGAACTCCAGTTTTGAAACCTCTCCT  
AAGAAAGTGAAATGGTCCAGCACCGTCACTCTCCCCGATTATCCCTCTTCTCAGATGGT  
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC  
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG  
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG  
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCACAGGGACAGTGCTGACAGAC  
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC  
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC  
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG  
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGGAAGAAGCTGTACTCGACCCCACTGCTGGCC  
ATCCCTACCTGCATGGGTTTCGGTGTTACCAGGACAAATACAGGTTCTTGGTGTTACCC  
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTGAGCCCAAAGCATGTGCTGTGACAG  
AGGTCTGTGCTGCAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCTCCATGAGAAT  
GAGTATGTTTCATGGAAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT  
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG  
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTATTAGCATGGAC  
CTGCACAAGGGATGCGGGCCCTCCCGCCGACGACCTCCAGAGCCTGGGCTACTGCATG  
CTGAAGTGGCTCTACGGGTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC  
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTAC  
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT  
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG  
CGTGTGCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

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## FIGURE 2EEEE

SEQ ID NO: 109\_S71575\_M VRK3\_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACAGGACAAGTACAGGTTCTAGTATTCC  
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG  
AGAGATGTGTFGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA  
ATGAGTATGTTACAGGGAACCTGACAGCTGAGAATGTCTTTGTGAATCCAGAGGATCTGA  
GCCAGGTGACCCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG  
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG  
ACCTGCACAAGGGATGCGGACCCTCCCGCCGACGCGATCTCCAGACCTTGGGCTACTGTA  
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA  
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC  
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGTATGGCCCTCAATT  
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA  
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG  
CTTCCGACTTGCAGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGA  
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA  
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTCATGTAATGTGAAACTCCTCCCTGTCTC  
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC  
TCCACTCCCTATGGCATTCTGTGTATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110\_AA45427\_H

ATGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAACTGTCATCATTGACAATAAGCGCTAC  
CTCTTCATCCAGAAACTGGGGGAGGGTGGGTTTCAGCTATGTGGACCTAGTGGAAGGGTTA  
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAG  
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC  
GTGGCTTACTGTCTGAGGGAAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC  
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG  
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCAT  
GCCAAGGGTTATGCCCACAGAGACTTGAAGCCCAACCAATATATTGCTTGGAGATGAGGGG  
CAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGGAGGGCTCC  
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC  
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTCTCGATGAGCGGACTGATGTCTGGTCC  
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTC  
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCAAAAGCCCCAGG  
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT  
CCTCACATTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA  
CATACTACCCAAATCTGA

SEQ ID NO: 111\_H05721\_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC  
GACGGCTGCGGGGGACCGGGCCGCGGCGCCACCATGGCGGTGCGACAGGCGCTGGGCCG  
CGGCTGACAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCAAGCCCGGCCGGGCTA  
CGGCTTGGGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC  
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT  
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTGTCAGCGGCAGTTCGTGGTGCGGGC  
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTCTGGCCTTCGGGCTAGGGCTGGG  
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA  
GGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTGACACGAGACGCTTGCA  
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGTCTG  
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACC  
GTTGCTTCCAGGGAGAGGCCAGGTACAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

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## FIGURE 2FFFF

GGGGGCCCCCTGCCTTCCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCCCTC  
CAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAGCGAGCCGAGTGGCCCTT  
GGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAGGTCCCAAGCAACTAGC  
CCCTCACCCCAACAATCATCCGGGTTCTCCGCGCCTTCACCTCTTCCGTGCCCTGCTGCC  
AGGGGCCCCCTGGTCGACTACCCCTGATGTGCTGCCCTCACGCCTCCACCCTGAAGGCCTGGG  
CCATGGCCGGACGCTGTTCCCTCGTTATGAAGAACTATCCCTGTACCCTGCGCCAGTACCT  
TTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGCTGCAGCTGCTGGAAGG  
CGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGAAATCCGACAACATCCT  
TGTGGAGCTGGACCCAGACGGCTGCCCCCTGGCTGGTGATCGCAGATTTTGGCTGCTGCC  
GGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGTACGTGGATCGGGGGCGG  
AAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCCGTCTGGCCCCAGGGCAGTAT  
TGAATACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCTATGAAATCTTCGGGCT  
TGTCATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCCGAGCTACCAAGAGGC  
TCAGCTACCTGCACTGCCCCGAGTCAGTGCCTCCAGACGTGAGACAGTTGGTGAGGGCACT  
GCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCCGAGTAGCCGCAAATGTGCTTCATCT  
AAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGTTAGACAAGATGGTTGG  
CTGGCTCTCCAAACAATCGGCCGCCACTTTGTTGGCCAAACAGGCTCACAGAGAAGTGTG  
TGTGGAACAACAAATGAAGATGCTCTTTCTGGCTAACCTGGAGTGTGAAACGCTCTGCCA  
GGCAGCCCTCTCTCTGCTCATGGAGGGCAGCCCTGTGATGTCCCTGCATGGAGCTGGT  
GAATTACTAAAAGAACATGGCATCCTCTGTGTCGTGATGGTCTGTGAATGGTGAGGGTGG  
GAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAAGGCTCGGGCTTGG  
CAAATGGAAGAACTTGAGTGAGAGTTTCACTGTCAGTCTCTGCTCACAGACATCTGAAA  
AGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGAGGGGTAGGCCTGCATC  
CACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAGTTTGGCTGTGACCTTT  
GCCCCAACACGAGGAACCTGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACCTG  
GATGAAGGCAGACATCAACATGGGTGAGCAGCTTCACTGAGTTACGGGAGTGGGAAATTACATG  
AGGCCTGGGCCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGCTACTGAATTATTAATC  
TCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTGTGGGGATTTAACTTGAG  
GGTTTCCCTCTGACTAGCCTCTCTTACAGGAATTGTGAAATATTAAATGCAAATTTACA  
ACTGCAGATGACGTATGTGCCCTTGAAGTGAATATTGGCTTTAAGAATGATTCTTCTTAT  
ACTCTGAAGGTGAGAATATTTTGTGGGCAGGTATCAACATTGGGGAGAGATTTTCAATGTC  
TAATAACTAATTTTATACATGATTTTGAAGCTATTGCCTAAATCAGCGTCAACATG  
CAGTAAAGGTTGTCTTCAACTGACAAA

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AATGAGATGGAGAAGTACGAGCGGATCCGAGTGGTGGGGAGAGGTGCCTTCGGGATTGTG  
CACCTGTGCCTGCGAAAGGCTGACCAGAAGCTGGTGATCATCAAGCAGATTCCAGTGGAA  
CAGATGACCAAGGAAGAGCGGCAGCCAGAAATGAGTGCCAGGTCCCTCAAGCTGCTC  
AACCACCCCAATGTCATTGAGTACTACGAGAACTTCTGGAAGACAAAGCCCTTATGATC  
GCCATGGAATATGCACCAGGCGGCACTCTGGCTGAGTTCATCCAAAAGCGCTGTAATTCC  
CTGCTGGAGGAGGAGACCATCCTGCACCTTCTTCGTGCAGATCCTGCTTGCACTGCATCAT  
GTGCACACCCACCTCATCCTGCACCGAGACCTCAAGACCCAGAACATCCTGCTTGACAAA  
CACCGCATGGTTCGTCAAGATCGGTGATTTCCGGCATCTCCAAGATCCTTAGCAGCAAGAGC  
ACCCCATGCTATATCTCCCTGAGCTGTGTGAGGGCAAGCCCTACAACCAGAAGAGTGAC  
ATCTGGGGCCCTGGGCTGTGCTCTACGAGCTGGCCAGCCTCAAGAGGGCTTTTCGAGGCT  
GCGAACTTGCCAGCACTGGTCTGAAGATCATGAGTGGCACCTTTGCACCTATCTCTGAC  
CGGTACAGCCCTGAGCTTCGCCAGCTGGTCTGAGTCTACTCAGCCTGGAGCCTGCCAG  
CGGCCACCACTCAGCCACATCATGGCACAGCCCTCTGCATCCGTGCCCTCTCAACCTC  
CACACCGACGGCAGAGAAGTCCGTGGCCCCCAGCAACACAGGGAGCAGGACCACAGTGT  
CCGCTGCAGAGAGGCATCATGACATTCCGGCAGCGGCAGCAATGGGTGCCTAGGCCAT

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## FIGURE 2GGGG

GGCAGCCTCACTGACATCAGCCAGCCCACCATTTGTGGAGGCTTTGTTGGGCTATGAAATG  
GTGCAGCAAGTGGAGGAGGCCCTGAGCTTCACTACTAGGCTCTGCACCCCTGGACCAG  
GAGCCTCTGCTGAGTATAGACCTGGGCACTGCTCACTCAGCTGCTGTGACTGGTGAGGAG  
GACTTGGGCTCTGGAGATGTAAACAGGTTACCCAGCTGGGAGAGAGGACATCTGCTGGCT  
GGTGTGGCGTCCAGCACTGATGTGTCTACCTTCTCTGAAGGTGACTGCAAGGAGCCTGAC  
AAGTGCTGCTGGAGACACAAGCAGTGCCTGGGCACATCATCTACCCCTTTCGCCTCTGAC  
TGTGTCCGCCACAGCCTGCACCTACACTCTGTCAACCACTGCAACTGTAATTCTAGGCTG  
AAGGACTCTTCAGAGGATAGCAGCAGCTCCCGGGGCGCGGGCCCAACCTGCTCCCATGTC  
ATCGAGTCCCCTTGCTTTGAGCTCACACCGGAGGAGGAGCATGTGGAGCGATTCCGGTAT  
GGCTGGTGCAAAAGCTACAGACCTGTCTGTGTGGCAGTGATCCACCATCCACTCTACCAT  
GAGTGTGGGGCAGATGATCTAAATGXAAAGAAGAGGAAGAGGAGGAGGAGGAAAAGCAAG  
CCCCCATCCCGACACAGGTGGGGCCCGCCACCGCCTCCCCTGACCTAGGCACAGCATG  
GCCACTGGTACCCCTGACTCCACAGCGCCCATCACCATCTGGCGCTCTGAGAGCCCCACA  
GGGAAGGGTCAGGGCAGCAAGGTGATCAAGAAGGTAAAGAAGAAAAAGGAAAAAGAGAAA  
GACAAGGAGGAGATGGATGAGAAGGCAAAGCTGAAGAAAAAGCCAAGAAAGGCCAGTTG  
ACTAAGAAGAAAAGCCCGGTTAAATTGGAGCCTTCCCCGCCAGACGTGAGCCGATCATT  
AGCGCAAGACAGCTGGCCAGGATGTCCGAGTCCAGCCCAGAAAGCCGGGAAGAGCTGGAG  
AGCGAGGACAGTTACAATGGCCGGGGGACAGGAGAACTGTCCAGCGAGGATATTGTGGAA  
TCATCATCGCCAGGAAGAGAGAGAAACAGTCCAGGCCAAAAAGACAGGGGCAAAGCCC  
TCACAAGCCAGGAAGGTAAACAAGAGAAAAATCTCCCCAGGATCAAACCCCAACCTCAGT  
TGAGGCCAGGGTGGTTCAGGGTGCAGAATAAATGCCATCGAGCCTGTGGCTGGCCCTCTGC  
TGCTGTTCTCTCCCTCCAACCTGGCTGTTTCTTGCGGGGCAAGGGGTGGGCTCAGGGCTG  
CAGGGGTTTCTCAAAGGCAATCCAGCTTTTCACAAAGGAAGCCCATGGGAAGGCAGGTGGG  
AGGGAAAGGAAGGGGCACAGCCCTATTTCTTCTACCTGCTAGGACAAGGTGGAAGAGTG  
TATCTGGGGTGGGAAGGAGGGCTTCCCCTCTCTGCTGCGAGAGACTGGTCTGTGTGAAAT  
CCACTTCTGGGACAGGCAGTACTGTCTGCAGCGATAACCCCAATAAACGGAACTTTTAA  
CCC

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ATGTCGGTGCTGGGGCAGTACGAGCGACACTGCGATTCCATCAACTCGGACTTTGGGAGC  
GAGTCCGGGGGTTGCGGGGACTCGAGTCCGGGGCCTAGCGCCAGTCAGGGGCCGCGAGCC  
GGCGGCGGCGCGGCGGAGCAGGAGGAACCTGCACTACATCCCCATCCGCGTCTGGGCCGC  
GGCGCCTTCGGGGAAGCCACGCTGTACCGCCGCACCGAGGATGACTCACTGGTTGTGTGG  
AAGGAAGTCGATTTGACCCGGCTGTCTGAGAAGGAACGTCGTGATGCCTTGAATGAGATA  
GTTATTCTGGCACTGCTGCAGCACGACAACATTATTGCCTACTACAATCACTTCATGGAC  
AATACCACGCTGCTGATTGAGCTGGAATATTGTAATGGAGGGAACCTGTATGACAAAATC  
CTTCGTCAGAAGGACAAGTTGTTTGAGGAAGAGATGGTGGTGTGGTACCTATTTTCAGATT  
GTTTCAGCAGTGAGCTGCATCCATAAAGCTGGAATCCTTCATAGAGATATAAAGACATTA  
AATATTTTTCTGACCAAGGCAAACCTGATAAACTTGGAGATTATGGCCTAGCAAAGAAA  
CTTAATTCTGAGTATTCCATGGCTGAGACGCTTGTGGGAACCCCATATTACATGTCTCCA  
GAGCTCTGTCAAGGAGTAAAGTACAATTTCAAGTCTGATATCTGGGCAGTTGGCTGCGTC  
ATTTTTGAACTGCTTACCTTAAAGAGGACGTTTGATGCTACAAACCCACTTAACCTGTGT  
GTGAAGATCGTGCAAGGAATTGCGGGCCATGGAAGTTGACTCTAGCCAGTACTCTTTGGAA  
TTGATCCAAATGGTTTCATTCGTGCCCTTGACCAGGATCCTGAGCAGAGACCTACTGCAGAT  
GAACTTCTAGATCGCCCTCTTCTCAGGAAACGCAGGAGGTCAAGCACTGTGACTGAAGCA  
CCCATTGCTGTAGTAACATCACGAACCAGTGAAGTCTATGTTTGGGGTGGTGGAAAATCC  
ACCCCCCAGAACTGGATGTTATCAAGAGTGGCTGTAGTGCCCGGCAGGTCTGTGCAGGG  
AATACCCACTTTGCTGTGGTTCACAGTGGAGAAGGAACTGTACACTTGGGTGAACATGCAA  
GGAGGCACTAACTCCATGGTCAGCTGGGCCATGGAGACAAAGCCTCCTATCGACAGCCA  
AAGCATGTGGAAGGTTGCAAGGCAAAGCTATCCGTCAGGTGTCATGTGGTGTGATGATTC



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## FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC  
ATGGGGGTGGACAAAGTTGCTGGCCCTGAAGTGCTAGAACCCATGCAGCTGAACTTCTTC  
CTCAGCAATCCAGTGGAGCAGGTCTCCTGTGGAGATAATCATGTGGTGGTTCTGACACGA  
AACAAGGAAGTCTATTTCTGGGGCTGTGGCGAATATGGACGACTGGGTTTGGATTTCAGAA  
GAGGATTATTATACACCACAAAAGGTGGATGTTCCCAAGGCCTTGATTATTGTTGCAGTT  
CAATGTGGCTGTGATGGGACATTTCTGTTGACCCAGTCAGGCAAAGTGCTGGCCTGTGGA  
CTCAATGAATTCAATAAGCTGGGTCTGAATCAGTGATGTCGGGAATTATCAACCATGAA  
GCATAACCATGAAGTTCCCTACACAACGTCCTTTACCTTGGCCAAACAGTTGTCCTTTTAT  
AAGATCCGTACCATTTGCCCCAGGCAAGACTCACACAGCTGCTATTGATGAGCGAGGCCGG  
CTGCTGACCTTTGGCTGCAACAAGTGTTGGGCAGCTGGGCGTTGGGAACTACAAGAAGCGT  
CTGGGAATCAACCTGTTGGGGGGACCCCTTGGTGGGAAGCAAGTGATCAGGGTCTCCTGC  
GGTGATGAGTTTACCATTGCTGCCACTGATGAGAAAGTATTGAATTCTAAGACCATCCGT  
TCCAATAGCAGTGGCTTATCCATTGGAAGTGTGTTTCAGAGCTCTAGCCCGGGAGGAGGC  
GGCGGGGGCGGCGGTGGTGAAGAAGAGGACAGTCAGCAGGAATCTGAAACTCCTGACCCA  
AGTGGAGGCTTCCGAGGAACAATGGAAGCAGACCGAGGAATGGAAGGTTTAATCAGTCCC  
ACAGAGGCCATGGGGAACAGTAATGGGGCCAGCAGCTCCTGTCTGGCTGGCTTCGAAAG  
GAGCTGGAATAATGCAGAATTTATCCCCATGCCTGACAGCCCATCTCCTCTCAGTGACGCG  
TTTTTCAGAATCTGAGAAAGATACCTTGCCCTATGAAGAGCTGCAAGGACTCAAAGTGGCC  
TCTGAAGCTCCTTTGGAACACAAACCCCAAGTAGAAGCCTCGGTAAGTGAAGCTTTTGGCC  
TTTGAATCACAACCTAGTCACCTCGGCTGAATCCTGCAGTAACCTGTGCTGGGAAGGGAAC  
ACCACTGACTCCTCCTGCGTGTGCGTGCAGCTCTCTGCAGGTGGAGGTTGA

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ATGAACCTGCTGCTCTCCTACCGCGATGTGCAGGACTACTCGGCCATCATTGAGCTGGTG  
GAGACGCTGCAGGCCTTGCCACCTGTGATGTGGCCGAGCAGCATAATGTCTGCTTCCAC  
TACACTTTTGCCCTCAACCGGAGGAACAGGCCTGGGGACCGGGCGAAGGCCCTGTCTGTG  
CTGCTGCCGCTGGTACAGCTTGAGGGCTCTGTGGCGCCCGATCTGTACTGCATGTGTGGC  
CGTATCTACAAGGACATGTTCTTCAGCTCGGGTTTCCAGGATGCTGGGCACCGGGAGCAG  
GCCTATCACTGGTATCGCAAGGCTTTTGACGTAGAGCCAGCCTTCACTCAGGCATCAAT  
GCAGCTGTGCTCCTCATTGCTGCCGGGCAGCACTTTGAGGATTCCAAGAGCTCCGGCTA  
ATAGGCATGAAGCTGGGCTGCCTGCTGGCCCGCAAAGGCTGCGTGGAGAAGATGCAGTAT  
TACTGGGATGTGGGTTTCTACCTGGGAGCCAGATCCTCGCCAATGACCCCAACCCAGGTG  
GTGCTGGCTGCAGAGCAGCTGTATAAGCTCAATGCCCCCATATGGTACCTGGTGTCCGTG  
ATGGAGACCTTCTGCTCTACCAGCACTTCAGGCCACGCCAGAGCCCCCTGGAGGGCCA  
CCACGCCGTGCCCACTTCTGGCTCCACTTCTTGCTACAGTCTCTGCCAACCATTCAAGACA  
GCCTGTGCCCAGGGCGACCAAGTGCTTGGTGCTGGTCTTGGAGATGAACAAGGTGCTGCTG  
CCTGCAAAGCTCGAGGTTCCGGGTACTGACCCAGTAAGCACAGTGACCCCTGAGCCTGCTG  
GAGCCTGAGACCCAGGACATTCCTTCCAGCTGGACCTTCCAGTCCGCTCCATATGCGGA  
GTCAGCGCCTCAAAGCGCGACGAGCGCTGCTGCTTCTCTATGCACTCCCCCGGCTCAG  
GACGTCCAGCTGTGCTTCCCCAGCGTAGGGCACTGCCAGTGGTTCTGCGGCCTGATCCAG  
GCCTGGGTGACGAACCCGGATTCCACGGCGCCCGCGGAGGCGGAGGGCGGGGGAG  
ATGTTGGAGTTTGATTATGAGTACACGGAGACGGGCGAGCGGCTGGTGCTGGGCAAGGGC  
ACGTATGGGGTGGTGTACGCGGGCCCGGATCGCCACACGAGGGTGCGCATCGCCATCAAG  
GAGATCCCGGAGCGGGACAGCAGGTTCTCTCAGCCCTGCATGAAGAGATCGCTCTTCAC  
AGACGCCTGCGCCACAAGAACATAGTGCGCTATCTGGGCTCAGCTAGCCAGGGCGGCTAC  
CTTAAGATCTTCATGGAGGAAGTGCTTGGAGGCAGCCTGTCTCCTTGCTGCGGTGCGGTG  
TGGGGACCCCTGAAGGACAACGAGAGCACCATCAGTTTCTACACCCGCCAGATCCTGCAG  
GGACTTGGCTACTTGCACGACAACACATCGTGACAGGGACATAAAAGGGGACAATGTG  
CTGATCAACACCTTCAGTGGGCTGCTCAAGATTTCTGACTTCGGCACCTCCAAGCGGCTG  
GCAGGCATCACACCTTGCACTGAGACCTTACAGGAACCTCTGCAGTATATGGCCCCAGAA

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## FIGURE 2III

ATCATTGACCAGGGCCCCACGCGGGTATGGGAAAGCAGCTGACATCTGGTCACTGGGCTGC  
ACTGTCAATTGAGATGGCCACAGGTGCCCCCCTTCCACGAGCTCGGGAGCCCCACAGGCT  
GCCATGTTTCAGGTGGGTATGTACAAGGTCCATCCGCCAATGCCAGCTCTCTGTCTGGCC  
GAGGCCCCAAGCCTTTCTCCTCCGAACTTTTGAGCCAGACCCCCGCTCCGAGCCAGCGCC  
CAGACACTGCTGGGGGACCCCTTCTGTCAGCTGGGAAAAGGAGCCGCAGCCCCAGCTCC  
CCACGACATGCTCCACGGCCCTCAGATGCCCCCTTCTGCCAGTCCCACTCCTTCAGCCAA  
TCAACCAACCCAGTCTCAGACATTCCCGTGCCCTCAGGCACCCCTCTCAGCACCCACCCAGC  
CCCCCGAAGCGCTGCCTCAGTTATGGGGGCACCAGCCAGCTCCGGGTGCCCGAGGAGCCT  
GCGGCCGAGGAGCCTGCGTCTCCGGAGGAGAGTTCCGGGGCTGAGCCTGCTGCACCAGGAG  
AGCAAGCGTCGGGCCATGCTGGCCGCAGTATTGGAGCAGGAGCTGCCAGCGCTGGCGGAG  
AATCTGCACCAAGGAGCAGAAGCAAGAGCAGGGGGCCCCGTCTGGGCAGAAACCATGTGGAA  
GAGCTGCTGCGCTGCCTCGGGGCACACATCCACACTCCCAACCGCCGCGCAGCTCGCCAG  
GAGCTGCGGGCGCTGCAAGGACGGCTGAGGGGCCAGGGCCTTGGGCCTGCGCTTCTGCAC  
AGACCGCTGTTTGCCTTCCCGGATGCGGTGAAGCAGATCCTCCGCAAGCGCCAGATCCGT  
CCACACTGGATGTTTCGTTCTGGACTCACTGCTCAGCCGTGCTGTGCGGGCAGCCCTGGGT  
GTGCTAGGACCGGAGGTGGAGAAGGAGGCGGTCTCACCGAGGTGAGAGGAGCTGAGTAAT  
GAAGGGGACTCCAGCAGAGCCCAGGCCAGCAGAGCCCGCTTCCGGTGGAGCCCGAGCAG  
GGCCCCGCTCCTCTGATGGTGCAGCTGAGCCTCTTGAGGGCAGAGACTGATCGGCTGCGC  
GAAATCCTGGCGGGGAAGGAACGGGAGTACCAGGCCCTGGTGACGGGGCTCTACAGCGG  
CTGAATGAGGAAGCCCGGACCTATGTCTGGCCCCAGAGCCTCCAACTGCTCTTTCAACG  
GACCAGGGCCTGGTGCAGTGGCTACAGGAACTGAATGTGGATTACAGGCACCATCCAAATG  
CTGTTGAACCATAGCTTCAACCTCCACACTCTGCTCACCTATGCCACTCGAGATGACCTC  
ATCTACACCCGCATCAGGGGAGGGATGGTATGCCGCATCTGGAGGGCCATCTTGGCACAG  
CGAGCAGGATCCACACCAGTCACCTCTGGACCCTGA

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ATGTTTGGGAAGAAAAAGAAAAAGATTGAAATATCTGGCCCGTCCAACTTTGAACACAGG  
GTTCACTACTGGGTTTGATCCACAAGAGCAGAAGTTTACCGGCCTTCCCCAGCAGTGGCAC  
AGCCTGTTAGCAGATACGGCCAACAGGCCAAAGCCTATGGTGGACCCTTCATGCATCACA  
CCCATCCAGCTGGCTCCTATGAAGACAATCGTTAGAGGAAACAAACCCTGCAAGGAAACC  
TCCATCAACGGCCTGCTAGAGGATTTTGACAAATCTCGGTGACTCGCTCCAACCTCCCTA  
AGGAAAGAAAGCCCCACCCACCCAGATCAGGGAGCCTCCAGCCACGGTCCAGGCCACGCG  
GAAGAAAATGGCTTCATCACCTTCTCCCAGTATTCCAGCGAATCCGATACTACTGCTGAC  
TACACGACCGAAAAGTACAGGGAGAAGAGTCTCTATGGAGATGATCTGGATCCGTATTAT  
AGAGGCAGCCACGCAGCCAAGCAAAATGGGCACGTAATGAAAATGAAGCACGGGGAGGCC  
TACTATTCTGAGGTGAAGCCTTTGAAATCCGATTTTGCCAGATTTTCTGCCGATTATCAC  
TCACATTTGGACTCACTGAGCAAACCAAGTGAATACAGTGACCTCAAGTGGGAGTATCAG  
AGAGCCTCGAGTAGCTCCCCTCTGGATTATTCAATTCCAATTACACCTTCTAGAACTGCA  
GGGACCAGCGGGTGCTCCAAGGAGAGCCTGGCGTACAGTGAAAGTGAATGGGGACCCAGC  
CTGGATGACTATGACAGGAGGCCAAAGTCTTCGTACCTGAATCAGACAAGCCCTCAGCCC  
ACCATGCGGCAGAGGTCCAGGTGAGGCTCGGGACTCCAGGAACCGATGATGCCATTTGGA  
GCAAGTGCAATTTAAAACCCATCCCCAAGGACACTCCTACAACCTCCTACACCTACCCTCGC  
TTGTCCGAGCCCACAATGTGCATTCAAAGGTGGATTACGATCGAGCACAGATGGTCCTC  
AGCCCTCCACTGTCAGGGTCTGACACCTACCCAGGGGGCCCTGCCAAACTACCTCAAAGT  
CAAAGCAAATCGGGCTATTCTCAAGCAGTCACCAGTACCCGTCTGGGTACCACAAAGCC  
ACCTTGTAACCATACCCCTCCCTGCAGAGCAGTTTCGCAGTACATCTCCACGGCTTCCTAC  
CTGAGCTCCCTCAGCCTCTCATCCAGCACCTACCCGCCGCCAGCTGGGGCTCCTCCTCC  
GACCAGCAGCCCTCCAGGGTGTCCCATGAACAGTTTCGGGCGGCCCTGCAGCTGGTGGTC  
AGCCCAGGAGACCCAGGGAATACTTGCCCAACTTTATCAAAATCGGGGAAGGCTCAACC  
GGCATCGTATGCATCGCCACCGAGAAACACACAGGGAAACAAGTTGCAGTGAAGAAAATG

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## FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAAGCTGCTTTTCAATGAGGTCGTGATCATGCGGGAT  
TACCACCATGACAATGTGGTTGACATGTACAGCAGCTACCTTGTGCGCGATGAGCTCTGG  
GTGGTCATGGAGTTTCTAGAAGGTGGTGCCTTGACAGACATTGTGACTCACACCAGAATG  
AATGAAGAACAGATAGCTACTGTCTGCCTGTCAGTTCTGAGAGCTCTCTCCTACCTTCAAT  
AACCAAGGAGTGATTACACAGGGACATAAAAAAGTGAAGTCCATCCTCCTGACAAGCGATGGC  
CGGATAAAGTTGTCTGATTTTGGTTTCTGTGCTCAAGTTTCCAAAGAGGTGCCGAAGAGG  
AAATCATTGGTTGGCACTCCCTACTGGATGGCCCCTGAGGTGATTTCTAGGCTACCTTAT  
GGGACAGAGGTGGACATCTGGTCCCTCGGGATCATGGTGATAGAAATGATTGATGGCGAG  
CCCCCTACTTCAATGAGCCTCCCCCTCCAGGCGATGCGGAGGATCCGGGACAGTTTACCT  
CCAAGAGTGAAGGACCTACACAAGGTTTCTTCAGTGCTCCGGGGATTCTTAGACTTGATG  
TTGGTGAGGGAGCCCTCTCAGAGAGCAACAGCCCAGGAAGTCCCTCGGACATCCATTCTTA  
AAACTAGCAGGTCCACCGTCTTGCATCGTCCCCCTCATGAGACAATACAGGCATCACTGA

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ATGAATGATAGGAATGAGATTCAAATGGAAGCCAAACTCCAAAGTCTTACCATTATAGCA  
CAGGAAATTCTATGCAGATTCTTTATTACCCTTAGGAGACATGCACGTTTCTTGCTCACT  
AAACTAGGAAGGCAAGGAATGGCAAGGTGAGGAATTACTCACAGCTGTGCTGTGTGCATT  
CTCTGTGGGCCTAGCAGGGAAGGGGACAGCCCTGTGGCAATGGGCATGACACGGATGCTC  
CTGGAATGCAGTCTCAGTGACAAGTTGTGTGTATCCAGGAGAAGCAGTATGAAGTGATT  
ATCGTCCCAACTTTGTTGGTTACTATCTTCCTCATCCTTCTTGGGGTCACTCTGTGGCTT  
TTTATCAGAGAACAAAGAACTCAACAGCAGCGTTCTGGACCTCAAGGCATTGCCCCCTGTT  
CCTCCACCTAGGGACCTAAGCTGGGAAGCAGGACATGGAGGAAATGTGGCTTTGCCACTT  
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GTGCCGCGGGAGCAACTCTCTGAAGTTCTGGAGCAGATTTGCAGTGGTAGCTGTGGGCCC  
ATCTTTTCGAGCCAATATGAACACTGGGGACCCTTCTAAGCCCAAGAGTGTTATTCTCAAG  
GCTTTAAAGAACACAGCTGGGCTCCATGAGGTACAAGATTTCTTAGGGCGAATCCAATTC  
CATCAATACCTGGGGAAACACAAAAACCTGGTGCAGCTGGAAGGCTGCTGCACTGAAAAG  
CTGCCACTCTATATGGTGTGGAGGATGTGGCCCAGGGGGACCTGCTCGGCTTTCTCTGG  
ACCTGTGCGCGGGATGTGATGACTATGGATGGTCTTCTCTATGATCTCACAGAAAAACAA  
GTATATCACATCGGAAAGCAAGTCCTTTTGGCGCTGGAATTCCTGCAGGAGAAGCATTG  
TTCCATGGGGATGTGGCAGCCAGGAATATTCTGATGCAAAGTGATCTCACTGCTAAGCTC  
TGTGGATTAGGCCTGGCTTATGAAGTTTACACCCGAGGGGCCATCTCCTCTACTCAAACC  
ATACCTCTCAAGTGCTTGGCCCCAGAACGGCTTCTCCTGAGACCTGCTAGCATCAGAGCA  
GATGTCTGGTCTTTTGGGATCCTGCTCTATGAGATGGTGACTCTAGGAGCACCACCGTAT  
CCTGAAGTCCCTCCTACCAGCATCCTAGAGCATCTCCAAAGAAGGAAAATCATGAAGAGA  
CCCAGTAGCTGCACACATACCATGTACAGTATCATGAAGTCCTGCTGGCGCTGGCGTGAG  
GCTGACCGCCCCCTACCTAGAGAGCTGCGCTTGGCGCTAGAAGCTGCCATTAAAACTGCA  
GATGACGAGGCTGTGTTACAAGTACCAGAGTTGGTGGTACCTGAACTGTATGCAGCTGTG  
GCCGGCATCAGAGTGGAGAGCCTCTTCTACAACCTATAGCATGCTTTGAAGAGTCTCGGGC  
AAGAAACATTTCATGCATGAGTATATGTTCTTGGGAATCAATTCCTCTAAGAACAGAGAATG  
GTCTTTCCCAGGGACACAAAGGGAGAAATGGGACATGGATTCTTGATCTTCCTTTACACA  
TTTCTCGGGAAATCTGAAATGATGCTGGATGGGACTCTACACATCCTGAGCTAAGACATA  
CTGTCACTCTCACTTCTGCTGTCCCAGTCCCTAGAAATCCTGGGTAGAAGTGGTGGACCTG  
TGCAAAGGAGGTTTTAGAACTCTGCAGTATTTGTTGGGGCATGGCACAAATAAGCTCATC  
CCTCCCGTCCGAGGCTAGTTTCTCTGGAACCAATTTTTATCTAGATGAAAATTTGGAA  
TGAAATGAAGGAATAGAAATCCAATAAAAGAGTTGAAGGGAAAGAAAATTTAAGGTTCTT  
CTTGCTCAGGATTACAGATATGGACCAACACCTCCTTCAAGAAAAGGTGGTAGGACACAA  
AGTTCTTCAGTCCCTGAGCCCTACATGTGGGGCTGGAGGAGAACTATAACGGAAAAACCTC  
TGAGTTTCACCTTAGGTATAGATAAAAGAAAGATGGTCCCCTTTTATCTGATTCTGAGAC  
AGGTAAATTCTGTTTGTACTACGTTTAATTAGAAGGTGGAGGAGTCATTTTCATGATTAA

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## FIGURE 2KKKK

GAACATTCAACATGTATTGTTTATTAGCTAGCTTCCTAGTTCCGATTAGACTAAGGAGA  
CTAAGCCTAGAGAGTCAATGTTAGAACAGTGAAGAATTCTGTGTGTGTGTGTGTGT  
GTGTGTGTGTGCACAATAAATAGGAAATGTAGAAACCAAGCAAGAAGGCTTAGTAGCTCA  
GTCTTTAA CAAGGGCTAGAAAAGAATGTAATCTGATATGGAAGGATAGCAGCTTCTAATT  
TTCAATCATCTGTTGATATACTGTGAACTTATTTTATTAAATTAATATTTATTAAATGG

SEQ ID NO: 117\_AA098024\_M

CTGCAGGAGAAGCACCTGTTTCATGGGGATGTGGCTGCCAGGAACATCCTGATCCAAAGT  
GACCTGACTCCCAAACCTTTGTCTATCTGGGCCTGGCTTATGAAGTTCATGCCCATGGGGCC  
ATCTCCTCTGCTCGATCCAGCACCATCCCTCTCAAGTGGCTTGCTCCAGAAAGGCTTCTC  
CTGAGACCTGCAAGCATCAGGGGAGATATTTGGTCTTTGGGATCCTGCTTTATGAGATG  
GTGACTCTAGGAGCACCACCATACCTGAAGTCCCTCCCACCAGCATCCTACAATATCTT  
CAGAGAAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG  
AAGTGCTGTTGGCGCTGGAGTGAGGACAGCCGCCCTTACTTGTTTCAAGCTGCTCCAGCGC  
CTAGAAGCTGCTTCTAGATCTGCCGATGACAAGGCTGTGTTGCAAGTGCCAGAGTTGGTG  
GTGCTGAACTGTATGCAGATGTGGCTGGCATCAGGGCAGAAAGCATTTCCCTATAGCTTC  
AGTGTCTTTTGAAGATGGTCTTAGACAAATGACTATATATGGGTGGAATTAGTTCCTTCA  
AGAACAGAGAGAAGGAACTTTCTGTGGCCACCAAGGGAGAAAAAAGGACATGGATCTTG  
CATCTTTCCCTAAACATTTTCTAGACATCTGAAATGCTGCTGGATGAAGCTCTACCTCT  
ACATACCATGTACTCTTGAGCTAAGAATCACCATCAATTGTAGTTTGCTTTCCAGTCCCA  
AGGGCTGAAGTATAAGTGGTGGACCGTGTCTATTCTAAAGGAGTTTTTAAATCTGCAAT  
GATTGTAAGGGAATTAGGCAAAGGGCTGGTCCCACTCACTCCAGGCTGGTTTACTACTG  
AAACTAGTTTTTCTTTTCTTTTTTTTAAAGTTAAACTATTACAGAGTAAAAATAAACCAG  
ATGGGCATGAATGAACACCTTCTAATTTTTTAACCATGAATTGAATATTGGAATTCATGAG  
AAAGAAAATTCTAGGTTCTTTTTTGCTAAGAGGTGTTAAGGTGAGTCAATATATCCTTCAA  
GGAAAGGCTTTGTCTCATCTATGTTGACGGGACGTAAAAGTCTCGTCCCGTTATGAAGA  
GCTGAAGAAGATCTATAAGAAACAATACTGAGCCTTTCCCTTGACTATAGATAGAAGAGCA  
TCCTTTTCAATTGAATCTGAGGCAGGTGGACCATGCATGATACTAAGTTTAATTAGAAGCA  
GGAGGAGTCATTTTATGATTAGGAACATTGTTTATCCCATTTGTTTGCCAGTTCCTGTAA  
GACTAAGGAGAATCAGCCTATAGAGCCAAAGCTAGAACCAGGGATAAAAAGTGTGTGTGT  
GTATAACAAATAGGAAGCATGAAAGTTCGAGCAAGAAGACTTAGTAACCCAGGTGGTCATT  
AAGAGGTACAGAGAAGAAGTAATCTTATAGGAATGGATGGTAGCTTCTAATTTTTTAACCA  
TTCATTGAAATAACTGTGAAGCAACTCATTAACTAGTATTTATTGACCAAAAGTAGACT  
TTTCAGGTGTATAGCTGCCAAAATCTCTATAATAAAGAGGCTAAAAGAAAATAAATGGGA  
GTTATTTTACTAGGAAAATTAGAGAACCTATAGTTTCCAAAAGAGATTCTTTATGTGCA  
AAATGAGATAACTCTCTACCTCACAGGGTTGGTGTGAGGAACAATGAGAAATATGTATTG  
TGTATTATGTAGAATATAATATATTCTCAATAAATACTAGTTTTTCCCCTTC

SEQ ID NO: 118\_SGK2ALPHA\_H

GAAGAGGGCAGAGCCGTGCATGGGGCTGCTCCCCAGGACCTGAGCAGGAACCTGGAGTTT  
TCAGAGCTGCCTGATCATTGCTACAGAATGAACTCTAGCCCAGCTGGGACCCCAAGTCCA  
CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCAG  
CCCACGGACTTCGACTTCCTCAAAGTCATCGGCAGGGAAGTACGGGAAGGTCTACTG  
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAGTCCATC  
TTAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG  
CGGCACCCCTTCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC  
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGTTT  
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC  
TCCCTCAACATCATTACAGGGATCTGAAACCAGAGAACATTCTCTTGGACTGCCAGGGA  
CACGTGGTGTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

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## FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT  
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGAGTCCCTCTACGAGATGCTCCATGGCCTG  
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA  
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG  
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC  
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA  
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG  
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA  
TTCTTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG  
ACCTGTGAAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA  
GAGCGACTCAAACATAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA  
AAGAAAAATAATGTTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC  
TGTATCTCTGCCCTGACCTTACCAATGGCTTCCAATGTTAGGTTTGCTACAAGATG  
GTTACTGGAGCTTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA  
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAAAGCTCCCCCAATGACTTTTGCTT  
CCATCTCTACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC  
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT  
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTGTTGGATTTTGATCT  
CAATGTGTAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTC  
TATGTTGAAAAA

SEQ ID NO: 120\_CCRK\_H

ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGGCGCCACGGCATCGTCTTCAAG  
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTTG  
GAAGACGGCTTCCCTAACCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC  
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC  
TTTGAGTTTCATGCTGTGCGATCTGGCCGAGGTGGTGCGCCATGCCAGAGGCCACTAGCC  
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCTCTTCTGCCATGCC  
AACAACTTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCCTCAGGCCAG  
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCCAGACGGCAGCCGCCTCTAC  
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC  
CCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC  
ACCCCAAACCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC  
TTTAAGGAGCAGGTGCCCATGCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCA  
TTGGATCTGCTGGGTCAATTCCTTCTCTACCTCCTCACCAGCGCATCGCAGCTTCCAAG  
GCTCTCCTCCATCAGTACTTCTTACAGCTCCCCTGCCTGCCATCCATCTGAGCTGCCG  
ATTCTCAGCGTCTAGGGGGACCTGCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT  
GACTTCCACGTGGACCGGCCTCTTGAGGGAGTGCCTGTTGAACCCAGAGCTGATTTCGGCC  
CTTCATCCTGGAGGGGTGAGAAGTTGGCCCTGGTCCCGTCTGCCTGCTCCTCAGGACCAC  
TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTCAACCTCCAAGGCCTCCCCATGGCC  
ACAGTGGGCCCCACACCACACCTTGGCCCTTAGCCCTTGCAGGGTTGGTCTCGAGGCAGA  
GGTCATGTTCCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTTCATGGCCT  
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT  
GCTGCCAGTCAAGGCCTGCATATGCAGAATGACGATGCCTGCCTTGGTGCTGCTTCCCC  
GAGTGCTGCCTCCTGGTCAAGGAGAAGTGACAGAGATAA

SEQ ID NO: 121\_TESK2\_H

GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC  
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA  
GTCTCCTCGTTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

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## FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC  
TCCCTCTTTGCCGCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC  
CTGCCTCAGTGTCAAACCAGAGAAGTAAATTCACAAAAATTTATGTGTGGAGTTC  
CTTCTTAAAAGAAGAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTCAA  
TTGCAGGATTTCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG  
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG  
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAAATAGGGTCTGGCTTCT  
TTTCTGAAGTGTTCAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA  
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT  
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA  
ACCTGCATTTGCCTTGGACTGTGAGGGTAAACTGGCCTATGACATAGCAGTGGGCCTCA  
GCTACCTTCACCTCAAAGGCATTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA  
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC  
CCGATGTCAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTTCCTTCTTATGGTATCA  
CTGAGGTTCTCCGAGATGAGCCCTATAATGAAAAGGCAGATGTGTTCTCTTATGGTATCA  
TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGACTATCTTCCCGCACAGAGA  
ATTTCCGGGCTGGACTATGATGCTTTCCAGCACATGGTGGGAGACTGTCCCCCAGATTTTC  
TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACCTGCGCCCATCTTTTGTGGAGA  
TTGGGAAGACCCTGGAGGAAATTCTGAGCCGCTACAGGAAGAAGAGCAGGAGGGATA  
GGAAGCTGCAGCCACAGCCAGGGGACTCTTGGAGAAAGCACCTGGGGTGAAGCGACTAA  
GCTCACTGGATGACAAGATCCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT  
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCCACGTACAGTGAGTGTCTTGGACC  
CATACTACCGGCCACGAGATGGTGCTGCCCGCACCCCCAAAGTCAACCCTTTTAGTGCTC  
GCCAGGACCTCATGGGGGGCAAGATCAAGTTTTTTTGACCTGCCCAGCAAGTCTGTCTCT  
CTCTGGTATTTGACCTGGATGCACCAGGGGCCGGAACATATGCCCTGGCTGACTGGCAGG  
AGCCCCCTGGCCCCACCTATTCGCCGTTGGCGTTCTTGGCTGGTTCGCCTGAGTCTTGC  
ATCAAGAGGCTTGTCCATTTGTGGGCCGGGAAGAATCGCTATCTGATGGGCCCCACCAC  
GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCCACCATTCCGGGCATCTGCCCTAC  
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAATGGTTTTG  
GGTCCAGGCCCCAGGGGACCAGTCCATGCCCTGCGGGTGCTTCTGAGGAGATGGAGGTAG  
AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAA  
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTAGTCCCTGCCTCACCTTGGGGATGGACCT  
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG  
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTCCCAGTGCCATTGGCTGTG  
TATGACGGGAGGCAGCAGTGAGAGGCCTTCTAGTTAGGGCCAACAGCTGATACCAAGCC  
TCTGAAATCCAGCAAGGAGGTCTGCCTCCCACCAGACCCTCTCCAGTGTACTTCCCCAGA  
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT  
TCCCCACCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA  
TGGAGCTGATCAAGAGGCCGTAATGGTTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT  
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCACCTTACTGCATGGTCAGAC  
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTTCATGGCTCTTAG  
CTAACCTATTCAAAGACCTTTTCTGTTGATTAATCTATTTTATATAAGGAGTC  
TTAATGTTCTGCCCCATAAGACTTTCAACCTTGTGGTGGGAGTGGGGCTGGTTTTGTAG  
GCCCTAGGGCCTGCTTCTATGTATTTATCAACATGTGATACATTCAATTGGTTAAATGGT  
TTATACAGGGACTGATTTGCTTCCCTTCCCTGCCATGGCTGGAGCTTTGGGAACAGTCTGT  
CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTATAACT  
TGCTTCTGTTGATTTTTTTTTTTGTAAACTTTCCCAAGACATTTTCAGACTTAAAAATAA  
AGTCAGTGTTACAGGT